

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:41:48 ; Search time 53.6679 Seconds
(without alignments)
826.886 Million cell updates/sec

Title: US-10-815-562-2_COPY_31_131
Perfect score: 535
Sequence: 1 QVLSYKEAVLRADIGNRS.....VTLNQARGSFDISCDKNR 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	100.0	140	8	ADJ82974 Human Pep
2	535	100.0	152	3	AAG03781 Human sec
3	535	100.0	169	8	ADK70797 Human CAP
4	535	100.0	170	2	AAR92924 Prepro-PA
5	535	100.0	170	3	AAB07901 A human c
6	535	100.0	170	5	ABB07707 Human pep
7	535	100.0	170	5	Aau90996 Transplan
8	535	100.0	170	7	ADP18219 Protein s
9	535	100.0	170	7	ADP65263 Human cat
10	535	100.0	170	8	Adi29582 Human CAP
11	535	100.0	170	8	ADJ82973 Human Pep
12	535	100.0	170	8	ADN41827 Human L-
13	535	100.0	170	8	ADR47315 Human cat
14	535	100.0	170	8	ABM80449 Tumour-as
15	535	100.0	170	9	ADW43827 Mouse che
16	535	100.0	170	9	ADX08374 Cathelic
17	535	100.0	170	9	ADZ80363 Human cat
18	475	88.8	177	4	Aau31061 Novel hum
19	408	76.3	170	9	AEA00315 Human cat
20	367	68.6	170	5	Aau90997 Transplan
21	367	68.6	170	9	ADX08375 Myeloid c
22	364	68.0	156	5	Aau90999 Transplan
23	364	68.0	156	9	ADX08377 Myeloid c
24	361	67.5	176	9	ADZ80368 Goat cath

25	354	66.2	155	5	ABB07704	Abb07704 Bovine pe
26	354	66.2	155	5	Aau90993	Aau90993 Transplan
27	354	66.2	155	5	ADX08371	Adx08371 Bactenecl
28	352.5	65.9	159	5	Aau90998	Aau90998 Transplan
29	352.5	65.9	159	5	ADX08376	Adx08376 BMAP-28 m
30	350	65.4	172	9	ADZ80367	Adz80367 PR-39 pol
31	347	64.9	147	2	AAW18158	Aaw18158 Antimicro
32	347	64.9	147	8	ADL18364	Adl18364 Pig prote
33	347	64.9	149	2	AAW25081	Aaw25081 Antimicro
34	347	64.9	149	2	AAW18157	Aaw18157 Antimicro
35	347	64.9	149	2	AAW18156	Aaw18156 Antimicro
36	347	64.9	149	2	AAW09087	Aaw09087 Antimicro
37	347	64.9	149	2	AAW18159	Aaw18159 Antimicro
38	347	64.9	149	8	ADL18362	Adl18362 Pig prote
39	347	64.9	149	8	ADL18366	Adl18366 Pig prote
40	347	64.9	149	8	ADL18368	Adl18368 Pig prote
41	343	64.1	142	8	ADK70796	Adk70796 Rabbit CA
42	343	64.1	171	5	ABB07703	Abb07703 Rabbit pe
43	340.5	63.6	160	5	AAU91000	Aau91000 Transplan
44	340.5	63.6	160	9	ADX08378	Adx08378 SMAP 29 a
45	340	63.6	176	5	ABB07705	Abb07705 Bovine pe

ALIGNMENTS

RESULT 1
ADJ82974
ID ADJ82974 standard; protein; 140 AA.
XX
AC ADJ82974;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Pep714-related peptide precursor SSQ ID NO: 2.
XX
KW pep714-related peptide; precursor; human; secreted peptide; Pep714;
KW oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
KW pneumonia.
XX
OS Homo sapiens.
XX
PN WO2004005338-A1.
XX
PD 15-JAN-2004.
XX
PF 30-JUN-2003; 2003WO-EP006930.
XX
PR 08-JUL-2002; 2002US-0394486P.
PR 07-JAN-2003; 2003US-0438602P.
(GENE-) GENEPROT INC.
PI Bougueleret L, Jeandenans C, Niknejad A;
XX
WPI; 2004-099371/10.
DR
PT Novel Pep714-related polypeptide having biological activity, useful for
PT treatment and prevention of microbial or viral infection, cystic fibrosis
PT and chronic respiratory infections.
XX
PS Disclosure; Page 92-93; 99pp; English.
XX
CC The present invention relates to a Pep714-related peptide. This is useful
CC for inhibiting microbial propagation, preferably viral propagation, and
CC in the treatment of chemotherapy and radiotherapy induced oral mucositis,
CC oral lesion, ventilator associated pneumonia, chronic respiratory
CC infections and cystic fibrosis. The present sequence is a Pep714-related
XX peptide precursor protein shown in the exemplification of the invention.
SQ Sequence 140 AA;
Query Match 100.0%; Score 535; DB 8; Length 140;

```
Best Local Similarity 100.0%; Pred. No. 9.6e-57;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
QY 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
DB 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101

RESULT 2
AAG03781
ID AAG03781 standard; protein; 152 AA.
XX
AC AAG03781;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 7862.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
DR N-PSDB; AAC03787.
XX
New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 13; SEQ ID NO 7862; 71pp + Sequence Listing; English.
XX
The present sequence is a polypeptide encoded by one of a large number of
5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 152 AA;

Query Match 100.0%; Score 535; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.1e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 34 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 93
QY 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101

Best Local Similarity 100.0%; Pred. No. 9.6e-57;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
QY 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
DB 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101

RESULT 3
ADK70797
ID ADK70797 standard; protein; 169 AA.
XX
AC ADK70797;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human CAPI8 full-length protein.
XX
KW alpha-helix; thionine; antibacterial; antifungal; plant;
KW fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
KW Pseudomonas; antimicrobial; rabbit; CAPI8.
XX
OS Homo sapiens.
XX
PN JP2003204794-A.
XX
PD 22-JUL-2003.
XX
PF 15-JAN-2002; 2002JP-00006607.
XX
PR 15-JAN-2002; 2002JP-00006607.
XX
PA (TOYW ) TOYOTA CHUO KENKYUSHO KK.
XX
DR WPI; 2004-102620/11.
XX
Antimicrobial polypeptide composition for a plant pathogen, comprises one
PT or more types of thionine and/or a polypeptide having an alpha helix
PT structure, as an active ingredient.
XX
PS Disclosure; SEQ ID NO 38; 27pp; Japanese.
XX
The invention relates to a novel polypeptide composition for preventing
disease in an organism which comprises one or more types of polypeptide
CC which have an alpha-helix structure and/or thionine component. The
CC composition of the invention demonstrates antibacterial and antifungal
CC activities and may be useful for preventing a disease in an organism, for
CC generating cultivated plants and in providing resistance to plant tissue
CC against fungi such as Pyricularia oryzae (rice blast fungus),
CC Ceratocystis fimbriata and bacteria such as Pseudomonas etc. The
CC composition has high antimicrobial activity at low concentration. The
CC current sequence is that of the rabbit CAPI8 full-length protein of the
CC invention.
XX
SQ Sequence 169 AA;

Query Match 100.0%; Score 535; DB 8; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRAIDGINORSSDANLYRLDLLDPRPTMDGDDPTPKPVSVFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
DB 91 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDKNR 131

RESULT 4
AAR92924
ID AAR92924 standard; protein; 170 AA.
XX
AC AAR92924;
XX
DT 06-JUN-1996 (first entry)
XX
```

DE Prepro-FALL-99.
 XX FALL-39; cathelin; antibiotic; antimicrobial; antibacterial.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..131
 FT Protein /label= Prepro-peptide
 FT Protein 132..170
 FT Protein /label= FALL-39

XX WO9608508-A1
 XX
 PD 21-MAR-1996.

XX PF 12-SEP-1995; 95WO-SE001030.
 XX PR 13-SEP-1994; 94SE-00003055.

XX PA (BOWA/) BOWAN H G.

XX PI Agerberth B, Gudmundsson GH, Gunne H;
 XX DR WPI; 1996-179899/18.
 XX DR N-PSDB; AAT18233.

XX Novel peptide antibiotic, FALL-39 - overcomes classical antibiotic
 PT resistance and is non-cytotoxic.
 XX Example 2; Fig 1; 26pp; English.

XX Novel cathelin-like prepro-FALL-39 (AAR92924) is the precursor of the
 CC antimicrobial, antibacterial agent FALL-39 (see AAR92923). It is the
 CC product of a cDNA clone (AAT18233) isolated from a human bone marrow cDNA
 CC library. FALL-39 includes a helical region (see AAR92922) that is
 CC required for biological activity. FALL-39 is useful therapeutically for
 CC inhibiting microbial growth in mammals, including humans, and is non-
 CC cytotoxic

XX SQ Sequence 170 AA;
 Query Match 100.0%; Score 535; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 60
 DB 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 90

QY 61 QQSPEDCDPKDGLVKRCMGVTTLNQARGSPDISCDKNKR 101
 DB 91 QQSPEDCDPKDGLVKRCMGVTTLNQARGSPDISCDKNKR 131

RESULT 5
 AAB07901
 ID AAB07901 standard; protein; 170 AA.

XX AAB07901;

XX 14-NOV-2000 (first entry)

XX A human cationic protein designated CAP18.

XX Human; cationic protein; lipopolysaccharide binding; anticoagulant;
 KW CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis;
 KW coagulation-related disorder; disseminated intravascular coagulation.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Protein 134..170

FT /note= "reactive nitrogen inhibitory protein"
 XX US6103888-A.
 XX PD 15-AUG-2000.

XX PF 01-JUN-1999; 99US-00322911.
 XX PR 17-JUL-1992; 92US-00916761.
 XX PR 17-JUL-1992; 92US-00916765.
 XX PR 15-JUL-1993; 93WO-US006731.
 XX PR 27-SEP-1994; 94US-00313681.
 XX PR 01-AUG-1996; 96US-00691280.
 XX PA (PANO-) PANORAMA RES INC.

XX PI Larrick JW, Wright SC, Hirata M;
 XX DR WPI; 2000-531989/48.
 XX DR N-PSDB; AAR59574.

XX Novel human cDNA encoding cationic proteins having lipopolysaccharide
 PT binding and anticoagulant activity, useful for treating and diagnosing
 PT gram negative sepsis and disseminated intravascular coagulation.

XX PS Disclosure; Col 29-30; 46pp; English.

XX The present sequence represents a human cationic protein, having
 CC lipopolysaccharide binding and anticoagulant activity. The polypeptide is
 CC designated CAP18. Amino acids 134-170 of CAP18 represent a reactive
 CC nitrogen inhibitory protein (RNIP). The CAP18 polynucleotide is useful for
 CC for producing cationic proteins. The CAP18 polypeptide is useful for
 CC treating and diagnosing lipopolysaccharide-associated conditions such as
 CC gram negative sepsis, and/or coagulation-related disorders, such as
 CC disseminated intravascular coagulation

XX SQ Sequence 170 AA;

Query Match 100.0%; Score 535; DB 3; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 60
 DB 31 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRPTMDGDDPTPKPVSTVKTVCPRRTT 90

QY 61 QQSPEDCDPKDGLVKRCMGVTTLNQARGSPDISCDKNKR 101
 DB 91 QQSPEDCDPKDGLVKRCMGVTTLNQARGSPDISCDKNKR 131

RESULT 6
 ABB07707
 ID ABB07707 standard; peptide; 170 AA.

XX ABB07707;

XX 10-JUN-2002 (first entry)

XX Human peptide antibiotic FALL-39 precursor sequence.

XX Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
 KW antigen presenting cell; adjuvant; human; antibiotic; FALL-39.

XX Homo sapiens.

XX WO200213857-A2.

XX PD 21-FEB-2002.

XX 17-AUG-2001; 2001WO-EP009529.

XX 17-AUG-2000; 2000AT-00001416.

XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX
PI Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
XX
DR WPI; 2002-269154/31.
XX
XX Vaccine for active immunization or for preparing an adjuvant for
PT enhancing an immune response to at least one antigen, comprises at least
PT one antigen and at least one cathelicidin derived antimicrobial peptide.
XX
XX Disclosure; Fig 1; 65pp; English.
XX
XX The invention relates to a vaccine comprising at least one antigen and at
CC least one cathelicidin derived antimicrobial peptide or its derivative.
CC The vaccine is useful for active immunization, especially of humans or
CC animals without protection against the specific antigen. The cathelicidin
CC derived antimicrobial peptide is useful in the preparation of an adjuvant
CC for enhancing the immune response to at least one antigen, where the
CC adjuvant enhances the uptake of at least one antigen in antigen
CC presenting cells (APC), and the adjuvant is added to the vaccine.
CC Sequences AB807701-07 represent cathelicidin proteins form various
CC species
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVLSYKKAVALRAIDGINQRSSDANLYRLLDLPRTMDGDDTPKPVSVFTVKETVCPRTT 60
Db 31 QVLSYKKAVALRAIDGINQRSSDANLYRLLDLPRTMDGDDTPKPVSVFTVKETVCPRTT 90
Qy 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKNKR 101
Db 91 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKNKR 131
RESULT 7
ID AAU90996 standard; peptide; 170 AA.
AC AAU90996;
XX
DT 05-JUN-2002 (first entry)
XX
XX Transplant media associated antimicrobial peptide #32.
XX
XX Transplant; antimicrobial peptide; pore forming agent;
KW cell surface receptor binding compound; kidney transplant; cardioplegia;
KW organ transplant; transplant rejection.
XX
XX Homo sapiens.
XX
XX WO200209738-A1.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 27-JUL-2001; 2001WO-US023785.
PF
XX
XX 28-JUL-2000; 2000US-0221632P.
PR
XX 17-NOV-2000; 2000US-0249602P.
PR
XX 15-MAY-2001; 2001US-0290932P.
PR
XX (MURPHY) MURPHY C J.
PA
XX
XX Murphy CJ, Reid TW, Mcanulty JP;
PI
XX
XX WPI; 2002-268995/31.
DR
XX
XX Media comprising antimicrobial polypeptides or pore forming agents and/or
PT cell surface receptor binding compounds useful for the storage and
PT

PT preservation of organs prior to transplant.
XX
XX Disclosure; Page 27; 78pp; English.
XX
XX The invention describes new transplant compositions comprising
CC antimicrobial polypeptides or pore forming agents and/or cell surface
CC receptor binding compounds. The media is capable of extending the
CC preservation period past 72 hours and can provide organs with increased
CC functionality upon transplant. animals receiving kidneys stored in the
CC media of the present invention for either three or four days had serum
CC creatinine levels of less than half of those observed in control animals
CC receiving kidneys stored in UW solution (defined in the specification)
CC alone. Lower serum creatinine levels are indicative of healthier kidneys
CC and a more preferable prognosis for the transplant patient. The media of
CC the invention are useful for decreasing the incidence and/or severity of
CC delayed graft function in patients receiving transplanted kidneys stored
CC and/or treated in the media. The media may also be used in procedures
CC such as cardioplegia. It is contemplated that transplant of healthier
CC organs leads to a decrease in chronic rejection. This sequence represents
CC an antimicrobial peptide studied in the development of the transplant
XX media
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVLSYKKAVALRAIDGINQRSSDANLYRLLDLPRTMDGDDTPKPVSVFTVKETVCPRTT 60
Db 31 QVLSYKKAVALRAIDGINQRSSDANLYRLLDLPRTMDGDDTPKPVSVFTVKETVCPRTT 90
Qy 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKNKR 101
Db 91 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKNKR 131
RESULT 8
ID ADF18219 standard; protein; 170 AA.
XX
AC ADF18219;
XX
DT 12-FEB-2004 (first entry)
XX
XX Protein sequence.
XX
XX Antimicrobial; LL-37; hCAP-18; antiarteriosclerotic; antiulcer;
KW vulnerary; cytostatic.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 6 /note= "Encoded by AAT"
FT
XX
XX EPI358888-A1.
PN
XX
XX 05-NOV-2003.
PD
XX
XX 27-FEB-2003; 2003EP-00004306.
PF
XX
XX 28-FEB-2002; 2002EP-00004656.
PR
XX
XX (BALS/) BALS R.
PA (KOCZ/) KOCZULLA A R.
PA (VDEG/) VON DEGENFELD G.
XX
XX Bals R, Koczulla AR, Von Degenfeld G;
PI
XX
XX WPI; 2003-879818/82.
DR
XX N-PSDB; ADF18220.
XX

PT Use of a peptide LL-37 for the preparation of a composition for
 PT preventing or treating wounds or a disease caused reduced blood flow,
 PT e.g. atherosclerosis, coronary heart disease, stroke, arterial occlusive
 PT diseases or ulcer.

XX Disclosure; Page; 15pp; English.

PS The present invention is based on the finding that human antimicrobial
 CC peptide LL-37 ADP18218 is capable of inducing functionally important
 CC angiogenesis in cell culture and in vivo by activation of the receptor
 CC molecule FRL1. LL-37 can be used in the preparation of a pharmaceutical
 CC composition for the prevention or treatment of a disease caused by, or
 CC resulting in, a reduced level of angiogenesis or arteriogenesis, or for
 CC the treatment of (infected) wounds or cancer. The disease may be
 CC associated with reduced blood flow, such as atherosclerosis, coronary
 CC heart disease, stroke, arterial occlusive disease or an ulcer.
 CC Suppression of angiogenesis through inhibition of LL-37 can be used to
 CC treat tumours, especially a carcinoma or sarcoma including cancer of the
 CC bile duct, brain, breast, colon, stomach, male and female reproductive
 CC organs, lung and airways, skin, gallbladder, liver, nasopharynx, nerve
 CC cells, kidney, prostate, and Kaposi's sarcoma (all claimed). The present
 CC protein sequence is not explained in the specification.

SQ Sequence 170 AA;

Query Match 100.0%; Score 535; DB 7; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTVKETVCPRTT 60
 DB 31 QVLSYKEAVLRADGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTVKETVCPRTT 90

QY 61 QQSPEDCDFKKGVLKRCMGVTTLNQARGSPDISCDKNKR 101
 DB 91 QQSPEDCDFKKGVLKRCMGVTTLNQARGSPDISCDKNKR 131

RESULT 9

ID ADP65263
 XX ADP65263 standard; protein; 170 AA.

AC ADP65263;

XX 12-AUG-2004 (first entry)

DE Human cathelicidin antimicrobial peptide. ✓

XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.

XX Homo sapiens.

OS WO2003072827-A1.

XX 04-SEP-2003. ✓

XX 31-OCT-2002; 2002WO-US035433.

XX 31-OCT-2001; 2001US-0336220P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Hirsch R, Thorton SL;

XX WPI; 2003-712740/67.

XX GENBANK; NP_004336.

PT Diagnosing and analyzing autoimmune disease using gene expression

PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.

XX Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing a
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This sequence represents a
 CC protein sequence relating to the genes used in the analysis and treatment
 CC of autoimmune diseases or arthritides. Note: This sequence is not shown
 CC in the specification. It has been supplied in an electronic format from
 CC WIPO.

SQ Sequence 170 AA;

Query Match 100.0%; Score 535; DB 7; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.2e-56;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTVKETVCPRTT 60

DB 31 QVLSYKEAVLRADGINQRSSDANLYRLDLLDPRPTMDGDDTPKPVSTVKETVCPRTT 90

QY 61 QQSPEDCDFKKGVLKRCMGVTTLNQARGSPDISCDKNKR 101

DB 91 QQSPEDCDFKKGVLKRCMGVTTLNQARGSPDISCDKNKR 131

RESULT 10

ID ADI29582
 XX ADI29582 standard; protein; 170 AA.

AC ADI29582;

XX 22-APR-2004 (first entry)

DE Human CAP18, SEQ ID 4.

XX CAP18; cationic antimicrobial protein of 18 kDa; bacterial pneumonia;
 KW chronic lung disease; acute lung disease; inflammatory lung disease;
 KW ARDS; bronchial asthma; human.

XX Homo sapiens.

XX WO2004009640-A1.

XX 29-JAN-2004.

XX 22-JUL-2003; 2003WO-JP009267.

XX 22-JUL-2002; 2002JP-00213040.

XX 14-MAR-2003; 2003JP-00070932.

PA (SEKG) SEIKAGAKU CORP.
PI Kirikae T, Toyooka K, Naiki Y, Tamura H, Ishizaka A, Hashimoto S;
XX WPI; 2004-143269/14.
XX New antibody against an antibacterial peptide, particularly human CAP18,
PT applicable in reagents and kits for detection, diagnosis and monitoring
XX of bacterial pneumonia.
XX
PS Disclosure; SEQ ID NO 4; 52pp; Japanese.
XX
CC The present invention relates to a novel CAP18 (cationic antimicrobial
CC protein of 18 kDa) antibody that can bind with human CAP18 peptide
CC fragments AD129579-AD129581. The antibody is useful in reagents and kits
CC for the detection, diagnosis and monitoring bacterial pneumonia and other
CC CAP18-related diseases like chronic and acute lung diseases, inflammatory
CC lung diseases, ARDS and bronchial asthma. The present sequence is human
CC CAP18.
XX
SQ Sequence 170 AA;
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDDPTPKPVSVFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKGVLKRCMGVTTLNQARGSPDISCDKDKNR 101
DB 91 QQSPEDCDFKKGVLKRCMGVTTLNQARGSPDISCDKDKNR 131
RESULT 11
ADJ82973
ID ADJ82973 standard; protein; 170 AA.
XX
AC ADJ82973;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Pep714-related peptide precursor SEQ ID NO: 1.
XX
KW pep714-related peptide; precursor; human; secreted peptide; Pep714;
KW oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
KW pneumonia.
XX
OS Homo sapiens.
FH Location/Qualifiers
FT 1..30
FT /label= signal_peptide
FT Protein 31..131
FT /label= propeptide
FT Cleavage-site 106..107
FT /note
FT /note= "dibasic peptidase cleavage site"
FT Cleavage-site 130..131
FT /note
FT /note= "dibasic peptidase cleavage site"
FT Protein 132..170
FT /label= antibacterial_protein_FALL-39
FT Protein 134..170
FT /label= antibacterial_protein_LL-37
FT Cleavage-site 140..141
FT /note
FT /note= "dibasic peptidase cleavage site"
FT Cleavage-site 151..152
FT /note
FT /note= "dibasic peptidase cleavage site"
XX

PN WO2004005338-A1.
XX
PD 15-JAN-2004.
XX
PF 30-JUN-2003; 2003WO-EP006930.
XX
PR 08-JUL-2002; 2002US-0394486P.
PR 07-JAN-2003; 2003US-0438602P.
XX
PA (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Jeandenans C, Niknejad A;
PI WPI; 2004-099371/10.
XX
XX Novel Pep714-related polypeptide having biological activity, useful for
PT treatment and prevention of microbial or viral infection, cystic fibrosis
PT and chronic respiratory infections.
XX
PS Disclosure; Page 91-92; 99pp; English.
XX
CC The present invention relates to a Pep714-related peptide. This is useful
CC for inhibiting microbial propagation, preferably viral propagation, and
CC in the treatment of chemotherapy and radiotherapy induced oral mucositis,
CC oral lesion, ventilator associated pneumonia, chronic respiratory
CC infections and cystic fibrosis. The present sequence is a Pep714-related
CC peptide precursor protein shown in the exemplification of the invention.
XX
SQ Sequence 170 AA;
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDDPTPKPVSVFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLPRTMDGDDPTPKPVSVFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKGVLKRCMGVTTLNQARGSPDISCDKDKNR 101
DB 91 QQSPEDCDFKKGVLKRCMGVTTLNQARGSPDISCDKDKNR 131
RESULT 12
ADN41827
ID ADN41827 standard; protein; 170 AA.
XX
AC ADN41827;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human LL-37 protein SEQ ID NO:2.
XX
KW infection; cathelicidin type peptide; LL-37; antimicrobial;
KW antiinflammatory; immunostimulant; bacterial infection; neutropenia;
KW toothpaste; mouthwash; gingivitis; oral infection; periodontitis; human.
XX
OS Homo sapiens.
XX
PN WO2004034061-A2.
XX
PD 22-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011240.
XX
PR 10-OCT-2002; 2002GB-00023655.
XX
PA (MABT-) MABTECH AB.
XX
PI Bonan H, Andersson M, Puetsep K, Carlsson G;
XX WPI; 2004-364936/34.
DR N-PSDB; ADN41826.

XX Determination of susceptibility of subject to infection comprising
PT detecting cathelicidin type peptide present in sample, optionally
PT comparing level of peptide in sample to control sample.
XX
PS Disclosure; SEQ ID NO 2; 40pp; English.
XX
XX The present invention describes a method for determining the
CC susceptibility of a subject to infection. The method comprises: (i)
CC providing a sample from a subject; (ii) detecting any cathelicidin type
CC peptide (LL-37) present in the sample; (iii) optionally comparing the
CC level of LL-37 in the sample to a control sample; (iv) determining the
CC susceptibility of the subject to infection (where no LL-37 or a low level
CC of LL-37 indicates that subject is susceptible to infection); and (v)
CC optionally administering an antimicrobial agent to reduce infection. Also
CC described is a product containing LL-37 and a cytostatic drug,
CC corticosteroid or growth factor (preferably recombinant granulocyte
CC colony stimulating factor (G-CSF) or GM-CSF). The product has
CC antimicrobial, antiinflammatory and immunostimulant activities. The
CC method can be used for determining the susceptibility of a subject to
CC infection such as bacterial infection (e.g. Actinobacillus
CC actinomycetemcomitans infection) and neutropenia, and for diagnosing
CC neutropenia (e.g. Kostmann morbus). The method is also useful in the
CC manufacture of a medicament in the form of toothpaste or mouthwash for
CC the preventative treatment of infection e.g. gingivitis, oral infection
CC (such as periodontitis), and for the treatment of neutropenia. The method
CC controls the normal flora in neutropenia and so combat infections. The
CC present sequence represents the proform of human LL-37, which is used in
CC the exemplification of the present invention.
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDPDTPKPVSTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDPDTPKPVSTVKETVCPRTT 90
QY 61 QQSPEDCDFKXGGLVKRCMGVTTLNQARGSPDISCDKNKR 101
Db 91 QQSPEDCDFKXGGLVKRCMGVTTLNQARGSPDISCDKNKR 131
RESULT 13
ADR47315
ID ADR47315 standard; protein; 170 AA.
XX
XX ADR47315;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human cationic antimicrobial protein-18.
XX
XX cystic pulmonary fibrosis; cationic antimicrobial protein; CAP18;
XX pulmonary disease.
XX
XX Homo sapiens.
OS
XX JP2004245842-A.
FN
XX 02-SEP-2004.
PD
XX 13-FEB-2004; 2004JP-00036471.
PF
XX 14-FEB-2003; 2003US-0447310P.
PR
XX (SEKG) SEIKAGAKU KOGYO CO LTD.
PA
XX WPI; 2004-629859/61.
DR
XX Evaluating cystic pulmonary fibrosis, by measuring cationic antimicrobial
PT

PT protein of 18 kDa (CAP18) quantity in biological sample, and evaluating
PT fibrosis by comparing measured quantity and quantity of CAP18 in control
PT sample.
XX
XX Disclosure; SEQ ID NO 4; 14pp; Japanese.
XX
XX The invention relates to a novel method for evaluating cystic pulmonary
CC fibrosis. The method comprises: measuring the quantity of cationic
CC antimicrobial protein of 18 kDa (CAP18) in the biological sample
CC collected from the individual; comparing the quantity of CAP18 measured
CC in the previous step and the quantity of CAP18 in a control sample; and
CC evaluating cystic pulmonary fibrosis by associating comparison of
CC obtained results. The invention further comprises: a kit for carrying out
CC the evaluating method, comprising a solid-phase component and an antibody
CC coupled with an antigenic peptide having a sequence of ADR47312, or a
CC solid-phase component comprising an immobilised antibody (first antibody)
CC which is coupled with the antigenic peptide, and the antibody (second
CC antibody) coupled with the antigenic peptide. The method or kit are
CC useful for evaluating cystic pulmonary fibrosis in an individual, where
CC the evaluation includes diagnosis for the presence or absence of a risk
CC of cystic pulmonary fibrosis, evaluation of serious or acute conditions,
CC or the evaluation of the advanced grade of the disease. The method
CC enables simple, cost-effective, rapid, highly sensitive and highly
CC accurate evaluation of the acute or serious conditions, or the
CC advancement of the pulmonary diseases. This sequence represents the human
CC CAP18 protein of the invention.
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDPDTPKPVSTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDPDTPKPVSTVKETVCPRTT 90
QY 61 QQSPEDCDFKXGGLVKRCMGVTTLNQARGSPDISCDKNKR 101
Db 91 QQSPEDCDFKXGGLVKRCMGVTTLNQARGSPDISCDKNKR 131
RESULT 14
ABM80449
ID ABM80449 standard; protein; 170 AA.
XX
XX ABM80449;
XX
XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO36373, SEQ:1129.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX tumour; diagnosis; cell proliferative disorder; breast cancer;
XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX central nervous system cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; melanoma; leukaemia; hybridisation probe;
XX chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic.
XX
XX Homo sapiens.
OS
XX WO2004030615-A2.
FN
XX 15-APR-2004.
PD
XX 29-SEP-2003; 2003WO-US028547.
PF
XX 02-OCT-2002; 2002US-0414971P.
PR
XX (GETH) GENENTECH INC.
PA
XX Wu TD, Zhang Z, Zhou Y;
PI

```
XX WPI; 2004-347921/32.
DR N-PSDB; ACN37923.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 1129; 7273pp; English.
PS
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 535; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDPTPKPSFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDPTPKPSFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKNKR 101
DB 91 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKNKR 131
RESULT 15
ADW43827
ID ADW43827 standard; peptide; 170 AA.
XX
XX AC ADW43827;
XX
XX 24-MAR-2005 (first entry)
XX
XX Mouse chemerin peptide SEQ ID NO 51.
XX
XX gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; dermatological;
KW hemostatic; inflammation; antiinflammatory; hematological disease;
KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.
XX
XX Mus musculus.
OS
XX WO2005000875-A2.
XX
XX 06-JAN-2005.
XX
XX 25-JUN-2004; 2004WO-EP006945.
XX
XX 25-JUN-2003; 2003US-00603566.
XX
```

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(EURO-) EUROSREEN SA.
Wittamer V, Communi D, Dethaux M, Parmentier M, Loison C;
Ooms FDR;
WPI; 2005-058121/06.
New Chemerin polypeptides, useful for diagnosing and treating a disease,
e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,
sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
Disease, or histiocytosis.
Example 2; SEQ ID NO 51; 183pp; English.
The invention describes a polypeptide (I) of up to 50 amino acids where
the polypeptide binds specifically to a chemerinR polypeptide. Also
described are: a nucleic acid sequence encoding (I); an expression vector
comprising the coding sequence of the nucleic acid; a transgenic animal
transfected with the expression vector; a (therapeutic) composition
comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid
sequence of (I); an antibody that selectively binds to (I); identifying
an agent that modulates the interaction between a Chemerin polypeptide
and a ChemerinR polypeptide; detecting the presence, in a sample, of an
agent that modulates the interaction between a Chemerin polypeptide and a
ChemerinR polypeptide in a sample; identifying an agent that modulates
the function of ChemerinR polypeptide; detecting the presence, in a
sample, of an agent that modulates the function of ChemerinR polypeptide;
diagnosing a disease or disorder characterized by dysregulation of
ChemerinR (polypeptide) signaling; a kit, for screening agents that
modulate the signaling activity of ChemerinR polypeptide or for
diagnosing a disease or disorder characterized by dysregulation of
ChemerinR polypeptide signaling, comprising an isolated ChemerinR
polypeptide, (I), an isolated polynucleotide encoding (I), a cell
transformed with a polynucleotide encoding (I), and its packaging
materials; a non-human mammal transgenic for a Chemerin polynucleotide
encoding (I); identifying an antibody inhibiting ChemerinR activation;
and an in vitro method of inhibiting cell proliferation. The
(therapeutic) composition or expression vector is useful for preparing a
medicament for ex vivo gene therapy or for in vivo gene therapy or a
medicament for inhibiting cell proliferation, where the medicament is
used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
lymphoproliferative diseases, disorders, and/or conditions,
paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's
Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other
hyperproliferative disease. The polypeptides and polynucleotides and
methods are useful for diagnosing and treating the cited diseases. This
is the amino acid sequence of a mouse chemerin peptide used to analyse
processing of immature chemerin.
SQ Sequence 170 AA;
Query Match 100.0%; Score 535; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDPTPKPSFTVKETVCPRTT 60
DB 31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDPTPKPSFTVKETVCPRTT 90
QY 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKNKR 101
DB 91 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSFDISCDKNKR 131
Search completed: January 12, 2006, 21:48:09
Job time : 53.6679 secs
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:43:14 ; Search time 8.94465 Seconds
(without alignments)
1086.448 Million cell updates/sec

Title: US-10-815-562-2_COPY_31_131
Perfect score: 535
Sequence: 1 QVLSYKEAVLRADINGNQRS.....VTLNQARGSPDISCDKNKR 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	100.0	170	2	I38932
2	530	99.1	170	2	S74248
3	366	68.4	155	2	S68229
4	361	67.5	153	2	A53421
5	354	66.2	155	2	S27018
6	350	65.4	172	2	S68232
7	350	65.4	212	2	S57330
8	347	64.9	147	2	JN0900
9	347	64.9	149	2	A53895
10	347	64.9	149	2	S57607
11	347	64.9	149	2	S53895
12	347	64.9	149	2	S57609
13	346	64.7	228	2	S40463
14	344	64.3	166	2	S41731
15	343	64.1	171	2	J01171
16	340.5	63.6	152	2	S68411
17	340	63.6	167	2	S68967
18	340	63.6	176	2	A45328
19	333.5	62.3	160	2	S68412
20	333.5	62.3	160	2	S68412
21	327	61.1	173	2	S70521
22	323	60.4	144	1	JC1222
23	319	59.6	96	1	XKPGC
24	312	58.3	190	2	S68230
25	146	27.3	135	2	B46634
26	144	26.9	137	2	A46634
27	85.5	16.0	200	2	I46051
28	85	15.9	434	1	KGBOL2
29	85	15.9	619	1	KGBOHI

30 84 15.7 436 1 KGBOL1
31 84 15.7 621 1 KGBOHI
32 79 14.8 263 2 C84397
33 73 13.6 355 2 T05390
34 72.5 13.6 211 2 G01654
35 72.5 13.6 332 2 S16586
36 71.5 13.4 364 2 G82903
37 69.5 13.0 329 2 S04132
38 69.5 13.0 332 2 T02066
39 69 12.9 427 1 KGHUL1
40 69 12.9 644 1 KGHUHI
41 68.5 12.8 331 2 T08403
42 68.5 12.8 1076 2 JC2217
43 68 12.7 673 2 S60173
44 66.5 12.4 312 2 G87536
45 66.5 12.4 332 2 S11852

ALIGNMENTS

RESULT 1

I38932
CAP18 precursor - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: I38932
R/Larrick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.
Infect. Immun. 63, 1291-1297, 1995
- A>Title: Human CAP18: a novel antimicrobial lipopolysaccharide-binding protein.
A/Reference number: I38932; MUID:95197251; PMID:7890387
A/Accession: I38932
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-170 <RES>
A/Cross-references: UNIPROT:P49913; UNIPARC:UPI0000000A67; EMBL:U19970; NID:G643476; PID
C/Superfamily: cathelin; cystatin homology
F:22-130/Domain: cystatin homology <CYS>

Query Match 100.0%; Score 535; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 QVLSYKEAVLRADINGNQRSSDANLYRLLDLPRTWDGDPDTPKPSFTVKETVCPRTT 60
|||||
Db 31 QVLSYKEAVLRADINGNQRSSDANLYRLLDLPRTWDGDPDTPKPSFTVKETVCPRTT 90
|||||

Cy 61 QQSPEDCDPKKQGLVKRCMGTVTNLNQRSGSPDISCDKNKR 101
|||||
Db 91 QQSPEDCDPKKQGLVKRCMGTVTNLNQRSGSPDISCDKNKR 131
|||||

RESULT 2

S74248
antibacterial peptide LL-37 precursor - human
N/Alternate names: antibacterial peptide FALL39
N/Contains: antibacterial peptide LL-37; cathelin-related antibacterial peptide CAP-18
C/Species: Homo sapiens (man)
C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C/Accession: S74248; S66281; S66205; A55596; S49441; S58023
R/Gudmundsson, G.H.; Agerberth, B.; Odeberg, J.; Bergman, I.; Olsson, B.; Salcedo, R.
Eur. J. Biochem. 238, 325-332, 1996
A>Title: The human gene FALL39 and processing of the cathelin precursor to the antibacte
A/Reference number: S74248; MUID:96283824; PMID:8691941
A/Accession: S74248
A/Molecule type: DNA
A/Residues: 1-170 <GUD>
A/Cross-references: UNIPROT:P49913; UNIPARC:UPI0000017636C; EMBL:X96735
A/Accession: S78211
A/Molecule type: protein
A/Residues: 134-143 <GUE>
A/Cross-references: UNIPARC:UPI0000017636D
R/Cowland, J.B.; Johnsen, A.H.; Borregaard, N.

Best Local Similarity 67.7%; Pred. No. 6.4e-31;
Matches 65; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTWMDGDPDTPKPVSFYTKETVCPRTT 60
DB 30 QALSYLEAVLRAVDQLNEQSSPNIYRLLELDPPQDDEDPDSFKRVSFYTKETVCSRTT 89

QY 61 QQSPEDCDPKKQGLVKKCMGTVTNLNQRGSFDISCD 96
DB 90 QQPPEQCDFKENGILLKRCGTVTLLDQVRGNFDITCN 125

RESULT 6

S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N;Alternate names: myeloid antibacterial protein PR-39
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68232; JN0899; I47138; S19563
R;Zhao, C.; Ganz, T.; Lehner, R.I.
FEBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophet
A;Reference number: S68232; MUID:56105365; PMID:7498526
A;Accession: S68232
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-172 <ZHA>
A;Cross-references: UNIPROT:P80054; UNIPARC:UPI000013215A; EMBL:X89201; NID:g1165150; PID:
R;Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the
A;Reference number: JN0899; MUID:94071853; PMID:8250863
A;Accession: JN0899
A;Molecule type: mRNA
A;Residues: 1-20, 'A', 22-172 <STO>
A;Cross-references: UNIPARC:UPI000016C6E7; GB:I23825; NID:G435100; PIDN:AAA31109.1; PID:
R;Experimental source: bone marrow cells
R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Bor
proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam
A;Reference number: I47138; MUID:95350216; PMID:7624374
A;Accession: I47138
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28, 'T', 30-89, 'OR', 92-116, 'NDP', 120-172 <GUD>
A;Cross-references: UNIPARC:UPI000016C6AC; EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PT
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall
Eur. J. Biochem. 202, 849-854, 1991
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of t
A;Reference number: S19563; MUID:92111534; PMID:1765098
A;Accession: S19563
A;Molecule type: protein
A;Residues: 131-169 <AGE>
A;Cross-references: UNIPARC:UPI000002D613
A;Experimental source: intestine
C;Genetics:
A;Gene: PR39
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial
P;1-29/Domain: signal sequence #status predicted <SIG>
P;22-129/Domain: cystatin homology <CVS>
P;130-130/Domain: propeptide #status predicted <PRO>
P;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>
P;169/Modified site: amidated carboxyl end (pro) stamides in mature form from following 91

Query Match 65.4%; Score 350; DB 2; Length 172;
Best Local Similarity 68.0%; Pred. No. 1.9e-30;
Matches 66; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTWMDGDPDTPKPVSFYTKETVCPRTT 60

[illegible]

RESULT 11

B53895
protegrin 4 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: B53895
R;Zhao, C.; Liu, L.; Lehrer, R. I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613; PMID:8013647
A;Accession: B53895
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPROT:P49933; UNIPARC:UPI00000131778; GB:X83258; NID:G603039; PIDN:
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status Predicted <SIG>
F;22-129/Domain: Cystatin homology <CVS>
F;131-148/Product: protegrin 4 #status Predicted <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following ql

Query Match	64.9%	Score	347;	DB	2;	Length	149;
Best Local Similarity	66.0%	Pred. No.	3.5e-30;				
Matches	64;	Conservative	17;	Mismatches	16;	Indels	0;
						Gaps	0;

Qy		1 QVLSYKEAVLRADIGINQRSSDANLYRLDLDPRTMGDDPTPKPVSFTVKETVCPRIT 60
		: : : :
Db		30 QALSYREAVLRADVRLNEOSSLNLYRLELDDPPKADEDGTPKPVSFTVKETVCPRPT 89

QY 61 QQSPECDFFKQDGLVKRCMGVTTLNQARGSFDISCDK 97
: || ||||: ||: ||||: : ||: :
Db 90 RPPELCDFKNGRVRKCVGVTLLDQKPLDITCNE 126

RESULT 12

S57609
protegrin 5 precursor - pig
N;Alternate names: cathelin-associated antimicrobial peptide
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S66283; S57609
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
A;Accession: S66283
A;Molecule type: DNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPROT:P49934; UNIPARC:UPI00000131779; EMBL:X84096; NID:9887646; PTD:
A;Experimental source: leukocytes

A:Gene: NPG5
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial
P;1-29/Domain: signal sequence #status predicted <SIG>
P;22-129/Domain: cystatin homology <CYS>
P;30-130/Domain: propeptide status predicted <PRO>
P;131-148/Product: protegrin 5 #status predicted <NAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide)

Query Match	64.9%	Score	347	DB 2	Length	149			
Best Local Similarity	66.0%	Pred. No.	3.5e-30						
Matches	64	Conservative	17	Mismatches	16	Indels	0	Gaps	0

Qy	1	QVLSYEAVLRAIDGINSQSSDANLYRLDLDPRTMGDDPDTKPVSTVTKETVCPRRT	60
Db	30	QALSYREAVLRAVDRUNEQSSSEANLYRLLELQDPKADDPGTPTVPSTVTKETVCPRPT	89
Qy	61	QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK	97
Db	90	ROPPELCLDFKENGKVCQGTVTLDQIKDPLDITNE	126

RESULT 13

S40463
prophenin (PP-2) precursor - pig
N:Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S40463; S57331; S68233
R:Pungarcar, J.; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk, V.
FEBS Lett. 336, 284-288, 1993
A:Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial
A:Reference number: S40463; MUID:94085623; PMID:8462247
A:Accession: S40463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-228 <PUN>
A:Cross-references: UNIPROT:P51525; UNIPARC:UPI00000131713; EMBL:X75438; NID:9443812; PID:
R:Strukelj, B.; Fungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V.
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A:Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
A:Reference number: S57330; MUID:96042752; PMID:7576250

A;Accession: S57331
A;Status: preliminary
A;Molecule type: mRNA

A: Cross-references: UNIPARC:UPI0000131713
 R: Zhao, C.; Ganz, T.; Lenner, R.I.
 FEBS Lett. 376, 130-134, 1995
 A: Title: Structures of ginsenosides for two cathelin-associated
 A: Reference number: S6832; PMID: 7498526
 A: Reference number: S6832; PMID: 96105365; PMID: 7498526

A;ACCESSION: S66233
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-228 <ZHA>

A/Cross-references: UNIPARC:UPI0000131713; EMBL:X89202; NID:g1116
C/Genetics:
A/Introns: 66/3; 102/3; 126/3
C/Superfamily: cathelin; cystatin homology
F/1-29/Domains: signal sequence #status predicted <SIG>
F/22-123/Domains: cystatin homology <CYS>
F/30-228/Product: prophenin (pp-2) #status predicted <MAT>

Query Match	Score 346;	DB 2;	Length 228;
Best Local Similarity	64.7%;		
Matches	63.4%;	Pred. No. 7.1e-30;	
64: Conservative	19;	Mismatches 18;	
		Indels	0: Gaps
			0:

Qy	1	QVL	S	K	E	A	V	L	R	A	I	D	G	I	N	Q	R	S	S	D	A	N	L	Y	L	L	D	L	D	P	R	P	T	M	D	G	D	P	D	T	K	P	S	P	T	V	K	E	T	V	C	P	R	T	60
dh	30	O	A	L	S	R	A	V	I	R	A	V	D	R	I	N	E	O	S	S	E	A	N	L	Y	L	L	E	L	D	O	P	P	K	A	D	E	D	G	T	K	P	S <td>P</td> <td>T <td>V</td> <td>K</td> <td>E</td> <td>T <td>V</td> <td>C</td> <td>P</td> <td>R</td> <td>T</td> <td>89</td> </td></td>	P	T <td>V</td> <td>K</td> <td>E</td> <td>T <td>V</td> <td>C</td> <td>P</td> <td>R</td> <td>T</td> <td>89</td> </td>	V	K	E	T <td>V</td> <td>C</td> <td>P</td> <td>R</td> <td>T</td> <td>89</td>	V	C	P	R	T	89

QY 61 QQSPEDCDFKKDGLVKRCMGVTTLNQARGSFDISCDKNKR 101

nb 90 RRPPELCDFKNGRVKOCVGVTLLDKPDLITCNEGVR 130

RESIST 14

antibacterial protein precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S41731
R/Storici, P.; Scocchi, M.; Tossi, A.; Gennaro, R.; Zanetti, M.
FEBS Lett. 337, 303-307, 1994
A/Title: Chemical synthesis and biological activity of a novel antibacterial

Recession, C. 72
Ristorici, P.; Scocchi, M.; Tossi, A.; Gennaro, R.; Zanetti, M.
FEBS Lett. 337, 303-307, 1994
A:Title: Chemical synthesis and biological activity of a novel antibacterial peptide de

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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:42:24 ; Search time 49.1956 Seconds
(without alignments)
1448.471 Million cell updates/sec

Title: US-10-815-562-2_COPY_31_131
Perfect score: 535
Sequence: 1 QVLSYKEAVLRADIGNORS.....VTLNQARGSFDISCDKNR 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_trembl.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	100.0	170	1 FAL39 HUMAN	P49913 homo sapien
2	535	100.0	170	1 FAL39 MACMU	Q718n9 macaca mula
3	503	94.0	170	2 Q9GLV5 MACMU	Q9GLV5 macaca mula
4	401	75.0	157	2 O62841 HORSE	O62841 equus cabal
5	367	68.6	170	2 O62842 HORSE	O62842 equus cabal
6	366	68.4	155	1 BCTN1 SHEEP	P54230 ovis aries
7	364	68.0	156	2 O62840 HORSE	O62840 equus cabal
8	361	67.5	153	1 PMP23 PIG	P49930 sus scrofa
9	361	67.5	176	1 BCTN5 SHEEP	P82018 capra hircu
10	361	67.5	176	1 BCTN5 SHEEP	P79362 ovis aries
11	361	67.5	176	2 O4JFB9 CAPRI	O4JFB9 capra hircu
12	354	66.2	155	1 BCTN1 BOVIN	P22226 bos taurus
13	352.5	65.9	159	1 BMA28 BOVIN	P54229 bos taurus
14	350	65.4	172	1 PR39 PIG	P80054 sus scrofa
15	350	65.4	212	1 PF11 PIG	P51524 sus scrofa
16	347	64.9	147	1 PG2 PIG	P32195 sus scrofa
17	347	64.9	149	1 PG1 PIG	P32194 sus scrofa
18	347	64.9	149	1 PG3 PIG	P32196 sus scrofa
19	347	64.9	149	1 PG4 PIG	P49933 sus scrofa
20	347	64.9	149	1 PG5 PIG	P49934 sus scrofa
21	346	64.7	228	1 PF12 PIG	P51525 sus scrofa
22	344	64.3	166	1 PMP16 PIG	P49931 sus scrofa
23	344	64.3	171	2 Q71KME RAT	Q71KME rattus norv
24	343	64.1	171	1 CAP18 RABIT	P25230 oryctolagus
25	340.5	63.6	160	1 SC51 SHEEP	P49928 ovis aries
26	340	63.6	167	1 PMP37 PIG	P49932 sus scrofa
27	340	63.6	176	1 BCTN5 BOVIN	P19660 bos taurus
28	339.5	63.5	165	1 BMA34 BOVIN	P56425 bos taurus
29	338.5	63.3	158	1 BMA27 BOVIN	P54228 bos taurus
30	334	62.4	158	2 Q9XSQB CAPRI	Q9XSQB capra hircu
31	333.5	62.3	160	1 SC52 SHEEP	P49929 ovis aries

32	333	62.2	190	1 BCTN7 BOVIN	P19661 bos taurus
33	332	62.1	172	2 Q6TN20 CANFA	Q6TN20 canis famil
34	327	61.1	173	1 CRAMP MOUSE	P51437 mus musculu
35	324	60.6	144	2 Q683R8 BUBBU	Q683R8 bubalus bub
36	323	60.4	144	1 INDC BOVIN	P33046 bos taurus
37	319	59.6	96	1 ICTL PIG	P15175 sus scrofa
38	318	59.4	164	2 P79361 SHEEP	P79361 ovis aries
39	318	59.4	190	2 Q9XSQB CAPRI	Q9XSQB capra hircu
40	316	59.1	165	2 P79360 SHEEP	P79360 ovis aries
41	312	58.3	190	1 BCTN7 SHEEP	P50415 ovis aries
42	308	57.6	224	2 O19031 SHEEP	O19031 ovis aries
43	303.5	56.7	165	2 P82017 CAPRI	P82017 capra hircu
44	299	55.9	182	2 O19040 SHEEP	O19040 ovis aries
45	280.5	52.4	178	2 Q91X12 CAVPO	Q91X12 cavia porce

ALIGNMENTS

RESULT 1
FAL39 HUMAN
ID FAL39 HUMAN STANDARD; PRT; 170 AA.
AC P49913;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein FAL39 precursor (FALL-39 peptide antibiotic)
DE (Cationic antimicrobial protein CAP-18) (hCAP-18) (HSD26) [Contains:
DE Antibacterial protein LB-37].
GN Name=CAMP; Synonyms=CAP18, FALL39;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE [MRNA], AND SYNTHESIS OF 132-170.
RC TISSUE=Bone marrow;
RX MEDLINE=95116523; PubMed=7529412;
RA Agerberth B., Gunne H., Odeberg J., Kogner P., Boman H.G.,
RA Gudmundsson G.H.;
RT "FALL-39, a putative human peptide antibiotic, is cysteine-free and
RT expressed in bone marrow and testis.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:195-199 (1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 42-68 AND 83-100.
RC TISSUE=Bone marrow;
RX MEDLINE=95339969; PubMed=7615076; DOI=10.1016/0014-5793(95)00634-L;
RA Cowland J.B., Johnsen A.H., Borregaard N.;
RA "hCAP-18, a cathelin/pro-bactenecin-like protein of human neutrophil
RT specific granules.";
RL FEBS Lett. 368:173-176 (1995).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Bone marrow;
RX MEDLINE=95197251; PubMed=7890387;
RA Larrick J.W., Hirata M., Balint R.F., Lee J., Zhong J., Wright S.C.;
RA "Human CAP18: a novel antimicrobial lipopolysaccharide-binding
RT protein.";
RL Infect. Immun. 63:1291-1297 (1995).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=97102716; PubMed=8946956; DOI=10.1016/S0014-5793(96)01199-4;
RA Larrick J.W., Lee J., Ma S., Li X., Francke U., Wright S.C.,
RA Balint R.F.;
RT "Structural, functional analysis and localization of the human CAP18
RT gene.";
RL FEBS Lett. 398:74-80 (1996).
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=8681941;
RA Gudmundsson G.H., Agerberth B., Odeberg J., Bergman T., Olsson B.,
RA Salcedo R.;

Ref 1-4 Ref

"The human gene FALL39 and processing of the cathelin precursor to the antibacterial peptide LL-37 in granulocytes."; Eur. J. Biochem. 238:325-332(1996).

[6] NUCLEOTIDE SEQUENCE [MRNA].
RA Gao Y., Huang Y.F., Xia X.Y.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

[7] NUCLEOTIDE SEQUENCE [MRNA].
RP TISSUE=Testis;
RC Wu N., Miao S.Y., Zhang X.D., Qiao Y., Liang G., Wang L.F.;
RA "A new spermatogenesis-related gene.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

[8] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schattner R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201).";
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

[9] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in bone marrow and testis and neutrophils.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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DR EMBL; Z38026; CAAB6115.1; -; mRNA.
DR EMBL; X89658; CAAB61805.1; -; mRNA.
DR EMBL; U19970; AAA74084.1; -; mRNA.
DR EMBL; U48795; AAC02634.1; -; Genomic DNA.
DR EMBL; X96735; -; NOT ANNOTATED CDS; Genomic DNA.
DR EMBL; AY162210; AAN78318.1; -; mRNA.
DR EMBL; AY251531; AAP20054.1; -; mRNA.
DR EMBL; CR457083; CAG33364.1; -; mRNA.
DR EMBL; CE541961; CAG46759.1; -; mRNA.
DR EMBL; BC055085; AAH55089.1; -; mRNA.
DR F01; I38932; I38932.
DR F01; S74248; S74248.
DR HSP; P32196; 1KW1.
DR Ensembl; ENSG00000164047; Homo sapiens.

DR HGNC; HGNC:1472; CAMP.
DR MIM; 600474; -.
DR GO; GO:0042742; P:defense response to bacteria; TAS.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidins; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 30
FT PROPEP 31 131
FT CHAIN 132 170
FT CHAIN 134 170
FT MOD_RES 31 31
FT DISULFID 86 97
FT DISULFID 108 125
FT CONFLICT 6
FT SEQUENCE 170 AA; 19301 MW; 055B07DCA95A7D16 CRC64;
SQ
Query Match 100.0%; Score 535; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 7e-49;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLSYKEAVLRADIGINORSSDANLYRLLDLPRTMDGDDPTPKPVSTVKETVCPRTT 60
DB 31 QVLSYKEAVLRADIGINORSSDANLYRLLDLPRTMDGDDPTPKPVSTVKETVCPRTT 90
QY 61 QQSPEDCDFFKDGKLVKRCMGVTTLNQARGSFDISCDKNKR 101
DB 91 QQSPEDCDFFKDGKLVKRCMGVTTLNQARGSFDISCDKNKR 131
RESULT 2
FALL39 MACMU STANDARD; PRT; 170 AA.
ID FALL39 MACMU STANDARD; PRT; 170 AA.
AC Q715N9;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein FALL-39 precursor (FALL-39 peptide antibiotic)
DE (Cationic antimicrobial protein CAP-18) (zhCAP-18) [Contains:
DE Antibacterial protein LL-37 (zhLL-37)].
DE Name=CAMP; Synonyms=CAP18, FALL39;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RX MEDLINE=21137962; PubMed=11238224; DOI=10.1128/CDLI.8.2.370-375.2001;
RA Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
RT "Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are close homologues of human molcules";
RL Clin. Diagn. Lab. Immunol. 8:370-375(2001).
CC -!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in epithelia of various organs. Most abundant peptide levels are found in organs lining outer or inner body surfaces, such as organs of the respiratory or gastrointestinal tract.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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CC

[illegible]

```
RL FEBS Lett. 457:459-464(1999).
DR EMBL; AJ224929; CAA12228.1; -; mRNA.
DR HSSP; P32196; 1KWI.
DR SNR; O62842; 30-130.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidin; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHLICIDINS_1; 1.
DR PROSITE; PS00947; CATHLICIDINS_2; 1.
DR Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 170 myeloid cathelicidin 3.
SQ SEQUENCE 170 AA; 19299 MW; 5C35F1FA2D112BC8 CRC64;

Query Match 68.6%; Score 367; DB 2; Length 170;
Best Local Similarity 68.0%; Pred. No. 5.9e-31;
Matches 68; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINQRSSDANLYRLDLPRTMDGDPDPKPVSVFTVKETVCPRTT 60
Db 30 QALSKEAVLRADVGLNQRSSDANLYRLDLPKGDSDTPKPVSVFMVKETVCPRTM 89

QY 61 QQSPEDCFKDGKGLVKRCMGTVTLNQARSGFDISCDNK 100
Db 90 KQTPEQCDPFKENGKLVQCVGTVIDPVKQYFDASCDPEQR 129

RESULT 6
BCTN1 SHEEP
ID BCTN1_SHEEP STANDARD; PRT; 155 AA.
AC P54230;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cyclic dodecapeptide precursor (Bactenecin 1) (Bac1).
GN Names=BAC1A; Synonyms=BODEN;
GN and
GN Names=BAC1B; Synonyms=BODEB;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow.
RX MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3;
RA Bagella L., Scocchi M., Zanetti M.;
RT "cDNA sequences of three sheep myeloid cathelicidins.";
RL FEBS Lett. 376:225-228(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Liver;
RX MEDLINE=98121317; PubMed=9461419; DOI=10.1016/S0378-1119(97)00569-6;
RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT "Localization and genomic organization of sheep antimicrobial peptides genes.";
RL Gene 206:85-91(1998).
CC -1- FUNCTION: Potent microbicidal activity, active against
CC Staphylococcus aureus and Escherichia coli (By similarity).
CC -1- SIMILARITY: Belongs to the cathelicidin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L46853; AAA85469.1; -; mRNA.
DR EMBL; U60595; AAB49710.1; -; Genomic_DNA.
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DR EMBL; U60596; AAB49711.1; -; Genomic_DNA.
DR PIR; S68229; S68229.
DR HSSP; P32196; 1KWI.
DR SNR; P54230; 30-130.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidin; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHLICIDINS_1; 1.
DR PROSITE; PS00947; CATHLICIDINS_2; 1.
DR Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 143 By similarity.
FT PEPTIDE 144 155 Cyclic dodecapeptide.
FT MOD_RES 30 30 Pyrrolidone carboxylic acid (By similarity).
FT DISULFID 85 96 By similarity.
FT DISULFID 107 124 By similarity.
FT DISULFID 146 154 By similarity.
SQ SEQUENCE 155 AA; 17648 MW; 1690638C791B1736 CRC64;

Query Match 68.4%; Score 366; DB 1; Length 155;
Best Local Similarity 69.8%; Pred. No. 6.8e-31;
Matches 67; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRADGINQRSSDANLYRLDLPRTMDGDPDPKPVSVFTVKETVCPRTT 60
Db 30 QVLSYKEAVLRADVQLNEQSSEPNYRLLELOPFDQDDPDPKPVSVFTVKETVCPRTT 89

QY 61 QQSPEDCFKDGKGLVKRCMGTVTLNQARSGFDISCD 96
Db 90 QQPPEQCDPFKENGKLVKRCMGTVTLNQARSGFDITCN 125

RESULT 7
O62840 HORSE
ID O62840_HORSE PRELIMINARY; PRT; 156 AA.
AC O62840;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Myeloid cathelicidin 1 precursor.
GN Name=eCATH-1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow.
RX MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
RA Scocchi M., Bontempo D., Boscolo S., Tomasinaig L., Giulotto E.,
RA Zanetti M.;
RT "Novel cathelicidins in horse leukocytes.";
RL FEBS Lett. 457:459-464(1999).
DR EMBL; AJ224927; CAA12226.1; -; mRNA.
DR HSSP; P32196; 1KWI.
DR SNR; O62840; 30-130.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidin; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHLICIDINS_1; 1.
DR PROSITE; PS00947; CATHLICIDINS_2; 1.
DR Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 156 Potential.
SQ SEQUENCE 156 AA; 17647 MW; BB8EA5D150288FFD CRC64;

Query Match 68.0%; Score 364; DB 2; Length 156;
Best Local Similarity 67.0%; Pred. No. 1.1e-30;
```

	Matches	67;	Conservative	13;	Mismatches	20;	Indels	0;	Gaps	0;
Qy	1	QVLSYKAVLR	AIDGII	NQRSSDANLYRLLDLDPRTWDGD	PDPDPKPVSFVTKEVCVRRTT	60				
Db	30	QALSYSKAVLR	AVDGLNQRSDENLYRLLLEDPLPKGD	KDSDFPKPVSFMVKETVCPRIM	89					
Qy	61	QQSPEDCDFKKDG	LVKRCMGVTTLN	NRQSFDISCDKNK	100					
Db	90	KQTPEQCDDFKENG	LKVCCGVTVILGPVKDHFDVSCGE	POR	129					

```

RESULT 8
PMP23_PIG STANDARD; PRT; 153 AA.
ID PMP23_PIG
AC P49930;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial peptide PMAP-23 precursor (Myeloid antibacterial peptide
DE 23).
DE Name=PMAP23;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxID=9823;
[1]
RN NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 131-153.
RP TISSUE=Bone marrow;
RC MEDLINE=94179144; PubMed=8132502;
RA Zanetti M., Storici P., Tossi A., Scocchi M., Gennaro R.;
RT "Molecular cloning and chemical synthesis of a novel antibacterial
RT peptide derived from pig myeloid cells.";
RL J. Biol. Chem. 269:7855-7858(1994).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Liver;
RA Zhao C., Lehrer R.I.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Exerts antimicrobial activity against both Gram-positive
CC and negative bacteria at concentrations of 2-16 micro molar. Its
CC activity appears to be mediated by its ability to damage bacterial
CC membranes.
CC -1- SIMILARITY: Belongs to the cathelicidin family.
-----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC EMBL; L26053; AAA31103.1; -; mRNA.
CC EMBL; Y16624; CAA76328.1; -; Genomic_DNA.
CC PIR; A53421; A53421.
CC HSP; P32196; LXKE.
CC SMR; P49930; 30-130.
CC InterPro; IPR001894; Cathelicidin.
CC PANTHER; PTHR10206; Cathelicidin; 1.
CC Pfam; PF00666; Cathelicidins; 1.
CC ProDom; PD001838; Cathelicidin; 1.
CC PROSITE; PS00946; CATHELICIDINS_1; 1.
CC PROSITE; PS00947; CATHELICIDINS_2; 1.
CC Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 130 Potential.
FT PEPTIDE 131 153 Antibacterial peptide PMAP-23.
FT MOD_RES 30 30 Pyrrolidone carboxylic acid (By
FT similarity).
FT FT 85 96 By similarity.
FT FT 107 124 By similarity.
SQ SEQUENCE 153 AA; 17486 MW; 7ADAA22B6C206000 CRC64;
Query Match 67.5%; Score 361; DB 1; Length 153;

```

Best Local Similarity 68.0%; Pred.No. 2.3e-30;
Matches 66; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVLVSKEAVLRADIGINORSSDANLYRLDLDPRTWGDGPDTPKPVSVFTVKETVCPRTT 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 30 QALSRYENVLRAVDRLNEQSSEANLYRLELDOPPKADEDPGTPKPVSVFTVKETVCPRT 89
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 61 QQSPEDCDFKKOGLVKRCMGVTTLNQARGSFDISCDK 97
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 90 RPPPELCDFKENGVRVQCVCVTTLKEIRGNFDTICNQ 126
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 9

BCTNS_CAPHI STANDARD; PRT; 176 AA.

ID BCTNS_CAPHI ID AC P82018;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Bactenecin 5 precursor (Bac5) (ChBac5).
OS Name=BAC5;
GN Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
[1]

NUCLEOTIDE SEQUENCE OF 131-149 AND 151-153, AND PROTEIN SEQUENCE.

TISSUE=Bone marrow, and Leukocyte;
MEDLINE=99346202; PubMed=10417180;
Shamova O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N.,
Lehrer R.I.;
RA "Purification and properties of proline-rich antimicrobial peptides
from sheep and goat leukocytes";
RL Infect. Immun. 67:4106-4111(1999).

-I- FUNCTION: Binds to the lipid A moiety of bacterial membrane of all Gram-negative bacteria. Shows a potent antimicrobial activity against Gram-negative bacteria E.coli, S.typhimurium and P.aeruginosa. Less active against Gram-positive bacteria S.aureus, L.monocytogenes and B.subtilis.

CC -I- DOMAIN: Bac5 sequence consists almost exclusively of X-P-P-Y repeats.

CC CC -I- PTM: Elastase is responsible for its maturation.

CC CC -I- SIMILARITY: Belongs to the cathelicidin family.

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HSSP; P32196; IWKI.
SMR; P82018; 30-130.
InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelcidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Amidation; Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrolidone carboxylic acid; Repeat; Signal.
FT SIGNAL 1 29
FT PROPSP 30 130
FT PEPTIDE 131 173
FT PROPEP 174 176
MOD_RES 30 30
FT FT
FT MOD_RES 173 173
FT FT
FT Bactenecin 5.
FT PEPTIDE 85 96
FT DISULPID 107 124 By similarity.
SQ SEQUENCE 176 AA; 19846 MW; 6FD7056C954E340A CRC64;

```

Query Match          67.5%; Score 361; DB 1; Length 176;
Best Local Similarity 68.0%; Pred. No. 2.7e-30;
Matches 66; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLLDLPRTMDGDDPTPKPVSFTVKETVCPRTT 60
   |||:|||||: :|||:|||||:|||||: :|||:|||||:|||||:
Db 30 QALSRYEAVLRAVGQLNRSSEANLYRLLELDPAPNDEVDPTGTRKPVSTVKETVCPRTT 89
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 90 QQPPECDKFENGLVKQCVGTTLDPNSNDQFDINCNE 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
BCTN5_SHEEP
ID ECTN5_SHEEP STANDARD; PRT; 176 AA.
AC P79362; P79363;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Bactenecin 5 precursor (Bac5) (OaBac5).
GN Name=BAC5;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
OX [1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RC TISSUE=Liver;
RX MEDLINE=9812117; PubMed=9461419; DOI=10.1016/S0378-1119(97)00569-6;
RA Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT "Localization and genomic organization of sheep antimicrobial peptides
   gene."
RL Gene 206:85-91(1998).
CC -!- FUNCTION: Binds to the lipid A moiety of bacterial
CC lipopolysaccharides (LPS), a glycolipid present in the outer
CC membrane of all gram-negative bacteria. Potent antimicrobial
CC activity (by similarity).
CC -!- DOMAIN: BAC5 sequence consists almost exclusively of X-P-P-Y
CC repeats.
CC -!- PTM: Elastase is responsible for its maturation (By similarity).
CC -!- SIMILARITY: Belongs to the cathelicidin family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; U60599; AAB49714.1; -; Genomic_DNA.
DR EMBL; U60601; AAB49716.1; -; mRNA.
DR HSSP; P32196; 1KW1.
DR SMR; P79362; 30-130.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidine; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS 1; 1.
DR PROSITE; PS00947; CATHELICIDINS 2; 1.
KW Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
KW Repeat; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 130 Bactenecin 5.
FT PEPTIDE 131 173 Removed in mature form.
FT PROPEP 174 176 Pyrrolidone carboxylic acid (By
FT MOD_RES 30 30 similarity).
FT MOD_RES 173 173 Proline amide (G-174 provides amide
FT DISULFID 85 96 group).
FT DISULFID 107 124 By similarity.

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FT CONFLICT 79 T -> R (in Ref. 1; AAB49716).
SQ SEQUENCE 176 AA; 19842 MW; 05080026EA6FD5F7 CRC64;

Query Match          67.5%; Score 361; DB 1; Length 176;
Best Local Similarity 68.0%; Pred. No. 2.7e-30;
Matches 66; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLLDLPRTMDGDDPTPKPVSFTVKETVCPRTT 60
   |||:|||||: :|||:|||||:|||||: :|||:|||||:|||||:
Db 30 QALSRYEAVLRAVGQLNRSSEANLYRLLELDPAPNDEVDPTGTRKPVSTVKETVCPRTT 89
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 90 QQPPECDKFENGLVKQCVGTTLDPNSNDQFDINCNE 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q4JFB9 CAPHI PRELIMINARY; PRT; 176 AA.
AC Q4JFB9;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Bac5 protein.
GN Name=bac5;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OC NCBI_TaxID=9925;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Bone marrow;
RX MEDLINE=99346202; PubMed=10417180;
RA Shanova O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N.,
RT "Purification and properties of proline-rich antimicrobial peptides
   from sheep and goat leukocytes."
RL Infect. Immun. 67:4106-4111(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RA Zhao C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y18873; CAC80206.1; -; mRNA.
SQ SEQUENCE 176 AA; 19846 MW; 6FD7056C954E340A CRC64;

Query Match          67.5%; Score 361; DB 2; Length 176;
Best Local Similarity 68.0%; Pred. No. 2.7e-30;
Matches 66; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVLSYKEAVLRAIDGINORSSDANLYRLLDLPRTMDGDDPTPKPVSFTVKETVCPRTT 60
   |||:|||||: :|||:|||||:|||||: :|||:|||||:|||||:
Db 30 QALSRYEAVLRAVGQLNRSSEANLYRLLELDPAPNDEVDPTGTRKPVSTVKETVCPRTT 89
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 QQSPEDCDFKKGDLVKRCMGVTTLNQARGSFDISCDK 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 90 QQPPECDKFENGLVKQCVGTTLDPNSNDQFDINCNE 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
BCTN1_BOVIN
ID ECTN1_BOVIN STANDARD; PRT; 155 AA.
AC P22226;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cyclic dodecapeptide precursor (Bactenecin 1) (Bac1).
GN Name=BAC1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.

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Db 30 QALSREAVLRAVDQLNKSSEANLYRLLELDPPPKEDDENFNIPKPSFRVKETVCPRT 89
QY 60 TQSPEDCPKDKGLVKRCMGVTTLNQARGSPDISC 95
Db 90 SQSPQCDPKFKNGLKRCVGTTLQVGSNFDITC 125

RESULT 14
PR39_PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein PR-39 precursor.
GN Name=PR39;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95350216; PubMed=7624374;
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
RT cathelin gene family member: comparative mapping of the locus for the
RT human peptide antibiotic FALL-39."
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089 (1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RC TISSUE=Bone marrow;
RX MEDLINE=94071853; PubMed=8250863;
RA Storici P., Zanetti M.;
RT "A cDNA derived from pig bone marrow cells predicts a sequence
RT identical to the intestinal antibacterial peptide PR-39."
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39."
RL FEBS Lett. 376:130-134 (1995).
RN [4]
RP PROTEIN SEQUENCE OF 131-169.
RC TISSUE=Intestine;
RX MEDLINE=92111534; PubMed=1765098;
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Mutt V., Joernvall H.;
RT "Amino acid sequence of proline-arginine-rich intestine of a new
RT member of the family of proline-arginine-rich antibacterial
RT peptides."
RL Eur. J. Biochem. 202:849-854 (1991).
RN [5]
RP PROTEIN SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophil;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha F.;
RT "Identification of a proline-arginine-rich antibacterial peptide from
RT neutrophils that is analogous to PR-39, an antibacterial peptide from
RT the small intestine."
RL J. Leukoc. Biol. 56:807-811 (1994).
CC -!- FUNCTION: Exerts a potent antimicrobial activity against both
CC E.coli and B.megaterium.
CC -!- TISSUE SPECIFICITY: Small intestine and bone marrow.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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CC removed.
CC -----
DR EMBL; X87236; CAA60682.1; -; Genomic_DNA.
DR EMBL; L23825; AAA31109.1; -; mRNA.
DR EMBL; X89201; CAA61487.1; -; Genomic_DNA.
DR PIR; S68232; S68232.
DR HSSP; P32196; 1KWI.
DR SMR; P80054; 30-130.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS 1; 1.
DR PROSITE; PS00947; CATHELICIDINS 2; 1.
KW Amidation; Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29
FT PROPEP 30 130
FT CHAIN 131 169
FT MOD_RES 30 30
FT MOD_RES 169 169
FT DISULFID 85 96
FT DISULFID 107 124
FT CONFLICT 21 21
FT CONFLICT 29 29
FT CONFLICT 90 91
FT CONFLICT 117 119
FT CONFLICT 157 157
SQ SEQUENCE 172 AA; 19477 MW; 994B792798C0E133 CRC64;

Query Match 65.4%; Score 350; DB 1; Length 172;
Best Local Similarity 68.0%; Pred.No. 3.9e-29;
Matches 66; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

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Db 30 QALSREAVLRAVDRLNEQSSEANLYRLLELDQPKADEDPGTPKPSFTVKETVCPRTT 89

QY 61 QQSPEDCPKDKGLVKRCMGVTTLNQARGSPDISCDK 97
Db 90 RQPELDCPKENGVRKQCVGTTLNPSIHSLDISCNE 126

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PF11_PIG STANDARD; PRT; 212 AA.
AC P51524;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prophenin-1 precursor (PF-1) (C6) (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=96042752; PubMed=7576250;
RA Strukelj B., Fungerear J., Kopitar G., Renko M., Lenarcic B.,
RA Berbic S., Turk V.;
RT "Molecular cloning and identification of a novel porcine cathelin-like
RT antibacterial peptide precursor."
RL Biol. Chem. Hoppe-Seyler 376:507-510 (1995).
RN [2]
RP PROTEIN SEQUENCE OF 131-209.
RC TISSUE=Blood;
RX MEDLINE=95212585; PubMed=7698355; DOI=10.1016/0014-5793(95)00210-Z;
RA Harwig S.S.L., Kokryakov V.N., Swiderek K.M., Aleshina G.M., Zhao C.,
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

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(without alignments)
533.455 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	535	100.0	170	2	US-09-322-911-2
4	535	100.0	170	2	US-09-917-340-32
5	367	68.6	170	2	US-09-917-340-33
6	364	68.0	156	2	US-09-917-340-35
7	354	66.2	155	2	US-09-917-340-29
8	352.5	65.9	159	2	US-09-917-340-34
9	347	64.9	147	1	US-08-243-879A-38
10	347	64.9	147	1	US-08-499-523-4
11	347	64.9	147	2	US-09-128-345-4
12	347	64.9	147	2	US-09-385-328-4
13	347	64.9	149	1	US-08-243-879A-36
14	347	64.9	149	1	US-08-243-879A-40
15	347	64.9	149	1	US-08-243-879A-42
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17	347	64.9	149	1	US-08-499-523-6
18	347	64.9	149	1	US-08-499-523-8
19	347	64.9	149	1	US-08-499-523-10
20	347	64.9	149	2	US-09-128-345-2
21	347	64.9	149	2	US-09-128-345-6
22	347	64.9	149	2	US-09-128-345-8
23	347	64.9	149	2	US-09-128-345-10
24	347	64.9	149	2	US-09-385-328-2
25	347	64.9	149	2	US-09-385-328-6
26	347	64.9	149	2	US-09-385-328-8
27	343	64.1	171	1	US-08-313-681A-4

28	343	64.1	171	2	US-09-322-911-4	Sequence 4, Appli
29	340.5	63.6	160	2	US-09-917-340-36	Sequence 36, Appl
30	340	63.6	176	2	US-09-917-340-28	Sequence 28, Appl
31	325	60.7	96	1	US-08-313-681A-5	Sequence 5, Appli
32	325	60.7	96	2	US-09-322-911-5	Sequence 5, Appli
33	314	58.7	59	2	US-09-621-976-7180	Sequence 7180, Ap
34	184	34.4	78	2	US-09-513-999C-4349	Sequence 4349, Ap
35	154	28.8	36	2	US-09-385-328-11	Sequence 11, Appl
36	126	23.6	66	2	US-09-385-328-10	Sequence 10, Appl
37	126	23.6	66	2	US-09-385-328-17	Sequence 17, Appl
38	75.5	14.1	1410	2	US-09-335-409-3	Sequence 3, Appli
39	75.5	14.1	1410	2	US-09-568-102-3	Sequence 3, Appli
40	75.5	14.1	1410	2	US-09-567-969-3	Sequence 3, Appli
41	75.5	14.1	1410	2	US-09-568-480-3	Sequence 3, Appli
42	75.5	14.1	1410	2	US-09-568-486-3	Sequence 3, Appli
43	75.5	14.1	1410	2	US-09-568-472-3	Sequence 3, Appli
44	75.5	14.1	1410	2	US-09-567-899-3	Sequence 3, Appli
45	75.5	14.1	1410	2	US-10-014-717-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-513-999C-7862
; Sequence 7862, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7862
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -33..-1
; OTHER INFORMATION: score 9.5
; OTHER INFORMATION: seq LLLGLVMPALIA/QV
US-09-513-999C-7862

Query Match 100.0%; Score 535; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 7e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 34 QVLSYKRAVLRAIDGINQRS DANLYRLLDLPRTWDGDPDTPKPSFTVKETVCPRTT 93

Qy 61 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSPDISCDKNKR 101

Db 94 QQSPEDCDFKKGGLVKRCMGVTTLNQARGSPDISCDKNKR 134

RESULT 2

US-08-313-681A-2
; Sequence 2, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; TITLE OF INVENTION: Human Cationic Proteins Having


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Best Local Similarity 100.0%; Pred. No. 8.2e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTWDGDDPTPKPVSFTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTWDGDDPTPKPVSFTVKETVCPRTT 90

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCDKNR 101
Db 91 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCDKNR 131

RESULT 5
US-09-917-340-33
; Sequence 33, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-917-340-33

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Best Local Similarity 68.0%; Pred. No. 1.7e-38;
Matches 68; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTWDGDDPTPKPVSFTVKETVCPRTT 60
Db 30 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTWDGDDPTPKPVSFTVKETVCPRIM 89

Qy 61 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCDKNK 100
Db 90 KQTPEQCDFKENGGLVKRCMGTVTILDPVKDYFDASCDSPQR 129

RESULT 6
US-09-917-340-35
; Sequence 35, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 156
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; TYPE: PRT
; ORGANISM: Equus asinus
US-09-917-340-35

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Best Local Similarity 67.0%; Pred. No. 3.6e-38;
Matches 67; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

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Qy 61 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCDKNK 100
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RESULT 7
US-09-917-340-29
; Sequence 29, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-29

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Best Local Similarity 67.7%; Pred. No. 6.6e-37;
Matches 65; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

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Qy 61 QQSPEDCDFKKGGLVKRCMGTVTILNQARGSFDISCD 96
Db 90 QQPPEQCDFKENGGLKCEGTVILDQVRGNFDITCN 125

RESULT 8
US-09-917-340-34
; Sequence 34, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 96
; LENGTH: 155
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; SOFTWARE: Patent in Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/09/128,345
; FILING DATE: 03-AUG-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-0054-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-128-345-4

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RESULT 12
US-09-385-328-4
; Sequence 4, Application US/09385328
; Patent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C.
; APPLICANT: Gu, Chee L.
; APPLICANT: Chen, Jie
; APPLICANT: Steinberg, Deborah A.
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
; APPLICANT: Kokryakov, Vladimir N.
; TITLE OF INVENTION: PROTEGRINS
; FILE REFERENCE: 8067-0067-999
; CURRENT APPLICATION NUMBER: US/09/385,328
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 09/128,345
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/741,860
; PRIOR FILING DATE: 1996-10-28
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Sus scrofa
; US-09-385-328-4

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Best Local Similarity 66.0%; Pred. No. 4.7e-36;
Matches 64; Conservative 17; Mismatches 16; Indels 0; Gaps 0;
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Db 30 QALSREAVLRADIGINQRSSDANLYRLDLDPRPTMDGDPDTPKPVSVFTVKETVCPRTT 89
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RESULT 13
US-08-243-879A-36
; Sequence 36, Application US/08243879A
; Patent No. 5708145
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: A NEW PROTEGRIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-243-879A-36

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Db 90 RPPPELDFKNGRVRKQCVGTITLDQIKDPLDITCNE 126

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RESULT 14
US-08-243-879A-40
; Sequence 40, Application US/08243879A
; Patent No. 5708145
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
; TITLE OF INVENTION: A NEW PROTEGRIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington, DC

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GenCore version 5.1.6
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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	535	100.0	170	5	US-10-844-837-32
5	535	100.0	170	5	US-10-777-683-4
6	535	100.0	170	5	US-10-909-119-47
7	535	100.0	170	5	US-10-657-851-32
8	535	100.0	170	5	US-10-893-485-51
9	535	100.0	170	5	US-10-287-436A-513
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13	367	68.6	170	5	US-10-909-119-48
14	367	68.6	170	5	US-10-657-851-33
15	364	68.0	156	3	US-09-917-340-35
16	364	68.0	156	5	US-10-844-837-35
17	364	68.0	156	5	US-10-909-119-50
18	364	68.0	156	5	US-10-657-851-35
19	354	66.2	155	3	US-09-917-340-29
20	354	66.2	155	4	US-10-344-709C-8
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22	354	66.2	155	5	US-10-909-119-44
23	354	66.2	155	5	US-10-657-851-29
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27	352.5	65.9	159	5	US-10-657-851-34

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28 347 64.9 147 3 US-09-539-443-4 Sequence 4, Appli
29 347 64.9 147 4 US-10-627-829-4 Sequence 4, Appli
30 347 64.9 149 3 US-09-539-443-2 Sequence 2, Appli
31 347 64.9 149 3 US-09-539-443-6 Sequence 6, Appli
32 347 64.9 149 3 US-09-539-443-8 Sequence 8, Appli
33 347 64.9 149 3 US-09-539-443-10 Sequence 10, Appli
34 347 64.9 149 4 US-10-627-829-2 Sequence 2, Appli
35 347 64.9 149 4 US-10-627-829-6 Sequence 6, Appli
36 347 64.9 149 4 US-10-627-829-8 Sequence 8, Appli
37 347 64.9 149 4 US-10-627-829-10 Sequence 10, Appli
38 343 64.1 171 4 US-10-344-709C-7 Sequence 7, Appli
39 340.5 63.6 160 3 US-09-917-340-36 Sequence 36, Appli
40 340.5 63.6 160 5 US-10-844-837-36 Sequence 36, Appli
41 340.5 63.6 160 5 US-10-909-119-51 Sequence 51, Appli
42 340.5 63.6 160 5 US-10-657-851-36 Sequence 51, Appli
43 340 63.6 176 3 US-09-917-340-28 Sequence 28, Appli
44 340 63.6 176 4 US-10-344-709C-9 Sequence 9, Appli
45 340 63.6 176 5 US-10-844-837-28 Sequence 28, Appli

```

ALIGNMENTS

RESULT 1

US-09-917-340-32

; Sequence 32, Application US/09917340

; Patent No. US2002090369A1

; GENERAL INFORMATION:

; APPLICANT: Murphy, Christopher J.

; APPLICANT: Meanulty, Jonathan P.

; APPLICANT: Reid, Ted W.

; TITLE OF INVENTION: Transplant Media

; FILE REFERENCE: TPLANT-06468

; CURRENT APPLICATION NUMBER: US/09/917,340

; CURRENT FILING DATE: 2001-07-29

; PRIOR APPLICATION NUMBER: 60/221,632

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 60/249,602

; PRIOR FILING DATE: 2000-11-17

; PRIOR APPLICATION NUMBER: 60/290,932

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 32

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-917-340-32

Query Match 100.0%; Score 535; DB 3; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.2e-52;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRADGINQRS DANLYRLDLLDPRPTWDGDDPTPKPVSYFTVKETVCPRTT 60

Db 31 QVLSYKEAVLRADGINQRS DANLYRLDLLDPRPTWDGDDPTPKPVSYFTVKETVCPRTT 90

Qy 61 QQSPEDCDFKXGVLVKRCMGVTTLNQARGSFDISCDKNKR 101

Db 91 QQSPEDCDFKXGVLVKRCMGVTTLNQARGSFDISCDKNKR 131

RESULT 2

US-10-603-566-51

; Sequence 51, Application US/10603566

; Publication No. US20040086968A1

; GENERAL INFORMATION:

; APPLICANT: Wittamer, Valerie

; APPLICANT: Communi, David

; APPLICANT: Vandenbogaerde, Ann

; APPLICANT: Detheux, Michel

; APPLICANT: Parmentier, Marc

; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin

```
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-603-566-51

Query Match      100.0%; Score 535; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 60
    |||||
Db  31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 90
    |||||

Qy  61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
    |||||
Db  91 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKDKNR 131
    |||||

RESULT 3
US-10-344-709C-11
; Sequence 11, Application US/10344709C
; Publication No. US20040170642A1
; GENERAL INFORMATION:
; APPLICANT: JORG FRITZ ET AL.
; TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin
; FILE REFERENCE: derived antimicrobial peptide or a derivative thereof
; FILE REFERENCE: SONN.030US
; CURRENT APPLICATION NUMBER: US/10/344,709C
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/EP01/09529
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: A 1416/2000
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; US-10-344-709C-11

Query Match      100.0%; Score 535; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 60
    |||||
Db  31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 90
    |||||

Qy  61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
    |||||
Db  91 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKDKNR 131
    |||||

RESULT 4
US-10-844-837-32
; Sequence 32, Application US/10844837
; Publication No. US20050014932A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
```

```
; APPLICANT: Imboden, Michael
; APPLICANT: Homan, Jane
; APPLICANT: Bremel, Robert D.
; TITLE OF INVENTION: Targeted Biocides
; FILE REFERENCE: IOGEN-09014
; CURRENT APPLICATION NUMBER: US/10/844,837
; CURRENT FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-844-837-32

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 60
    |||||
Db  31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 90
    |||||

Qy  61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
    |||||
Db  91 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKDKNR 131
    |||||

RESULT 5
US-10-777-683-4
; Sequence 4, Application US/10777683
; Publication No. US20050032117A1
; GENERAL INFORMATION:
; APPLICANT: Richard B. Moss
; APPLICANT: Akitoshi Ishizaka
; APPLICANT: Teruo Kiriakae
; TITLE OF INVENTION: Method for Assessment of Cystic Lung Fibrosis
; FILE REFERENCE: Q74236
; CURRENT APPLICATION NUMBER: US/10/777,683
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/447,310
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-777-683-4

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 60
    |||||
Db  31 QVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMDGDDTPKPVSVFTVKETVCPRTT 90
    |||||

Qy  61 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKDKNR 101
    |||||
Db  91 QQSPEDCDFKKGGLVKRCMGTVTLNQARGSFDISCDKDKNR 131
    |||||

RESULT 6
US-10-909-119-47
; Sequence 47, Application US/10909119
; Publication No. US20050079578A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
```



```

; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 47
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-119-47

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLDPRPTMDGDDPTPKPVSFTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINORSSDANLYRLDLDPRPTMDGDDPTPKPVSFTVKETVCPRTT 90

Qy 61 QQSPEDCDPCKDGLVKRCMGVTTLNQARGSPDISCDKDKNR 101
Db 91 QQSPEDCDPCKDGLVKRCMGVTTLNQARGSPDISCDKDKNR 131

RESULT 7
US-10-657-851-32
; Sequence 32, Application US/10657851
; Publication No. US20050089836A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/10/657,851
; CURRENT FILING DATE: 2003-09-09
; PRIOR FILING DATE: US/09/917,340
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-851-32

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLDPRPTMDGDDPTPKPVSFTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINORSSDANLYRLDLDPRPTMDGDDPTPKPVSFTVKETVCPRTT 90

Qy 61 QQSPEDCDPCKDGLVKRCMGVTTLNQARGSPDISCDKDKNR 101
Db 91 QQSPEDCDPCKDGLVKRCMGVTTLNQARGSPDISCDKDKNR 131

RESULT 8
US-10-893-485-51
; Sequence 51, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc

```

```

; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-51

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLDPRPTMDGDDPTPKPVSFTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINORSSDANLYRLDLDPRPTMDGDDPTPKPVSFTVKETVCPRTT 90

Qy 61 QQSPEDCDPCKDGLVKRCMGVTTLNQARGSPDISCDKDKNR 101
Db 91 QQSPEDCDPCKDGLVKRCMGVTTLNQARGSPDISCDKDKNR 131

RESULT 9
US-10-287-436A-513
; Sequence 513, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-513

Query Match      100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVLSYKEAVLRAIDGINORSSDANLYRLDLDPRPTMDGDDPTPKPVSFTVKETVCPRTT 60
Db 31 QVLSYKEAVLRAIDGINORSSDANLYRLDLDPRPTMDGDDPTPKPVSFTVKETVCPRTT 90

Qy 61 QQSPEDCDPCKDGLVKRCMGVTTLNQARGSPDISCDKDKNR 101
Db 91 QQSPEDCDPCKDGLVKRCMGVTTLNQARGSPDISCDKDKNR 131

RESULT 10
US-10-287-436A-1204
; Sequence 1204, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER

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RESULT 12
US-10-844-837-33
; Sequence 33, Application US/10844837
; Publication No. US20050014932A1
; GENERAL INFORMATION:
; APPLICANT: Imboden, Michael

```

RESULT 14
US-10-657-851-33
; Sequence 33, Application US/10657851
; Publication No. US20050089836A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/10/657,851
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/917,340
; PRIOR FILING DATE: 2001-07-29

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Search completed: January 12, 2006, 21:54:02
Job time : 41.7417 secs

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Db 141 DGNLYLLDMG-----SGTIK-----VKATQKANDGEWHYVDIQDGR-- 179
Qy 77 RCMGTVTILNQARSGFDISCDK 98
Db 180 --SGTISVNSRRTPPTASGESE 199

RESULT 2
US-11-000-463-348
; Sequence 348, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-348

Query Match 11.4%; Score 61; DB 7; Length 1091;
Best Local Similarity 25.8%; Pred. No. 21;
Matches 22; Conservative 11; Mismatches 21; Indels 28; Gaps 4;

Qy 22 DANLYRLDLDPRMTDGDPTPKVPSFTVKETVCPRTTQOSPED-----CDFKKDGLVK 76
Db 141 DGNLYLLDMG-----SGTIK-----VKATQKANDGEWHYVDIQDGR-- 179
Qy 77 RCMGTVTILNQARSGFDISCDK 98
Db 180 --SGTISVNSRRTPPTASGESE 199

RESULT 3
US-11-147-047-47
; Sequence 47, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
```

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; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-47

Query Match 11.2%; Score 60; DB 7; Length 349;
Best Local Similarity 28.4%; Pred. No. 6.5;
Matches 19; Conservative 6; Mismatches 30; Indels 12; Gaps 2;

Qy 22 DANLYRLDLDPRMTDGDPTPKVPSFTVKE-----TVCPRTTQOSPEDCDFKKDGLVKR 77
Db 234 DENSSAGLDIPGPPCTKASPEPAKPKFGASPEPEPSTACPKQKRRPAS-----VRR 285
Qy 78 CMGTVTIL 84
Db 286 AMGTVII 292

RESULT 4
US-10-467-657-3750
; Sequence 3750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3750
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3750

Query Match 11.1%; Score 59.5; DB 6; Length 389;
Best Local Similarity 26.8%; Pred. No. 8.6;
Matches 22; Conservative 10; Mismatches 31; Indels 19; Gaps 3;

Qy 6 KEAVLRAIDGINQRSSDANLYRLI-----DLDPRTWDGDDPTPKVPSFTVKETVCPRTT 60
Db 302 KEAAQTAVELVRRKPKDLNGVRLGLKLSLDPAWKADAD-----MMRSVIGRQL 351
Qy 61 QOSP-----EDCDFKKDGLVKRC 78
Db 352 QRSVMYRCRNCHFKASQVFFWHC 373
```

```
RESULT 5
US-11-055-822-68
; Sequence 68, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 68
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-68

Query Match 11.1%; Score 59.5; DB 7; Length 468;
Best Local Similarity 32.1%; Pred. No. 11;
Matches 18; Conservative 9; Mismatches 20; Indels 9; Gaps 2;

Qy 3 LSYKEAVLRADGINQR-----SSDANLYRLDLLDPRPTMGD-----PDTKPVSP 49
Db 315 LTLSSAVARSLGMLRMVQLALSSVERIFVIDLQPERTDPAHPLSLPDTPLGLSP 370

RESULT 6
US-10-667-295-43
; Sequence 43, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(102)

US-10-667-295-43

Query Match 10.8%; Score 58; DB 6; Length 141;
Best Local Similarity 23.3%; Pred. No. 3.6;
Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps 2;

Qy 8 AVLRAIDGINQRSSDANLYRLDLLDPRPTMGDPTPKPVSFYKVTVCPRTTQOSPDC 67
Db 74 SVVGAVDGV-----AMEVDVDSAK-----TNSNSDK 101

RESULT 7
US-10-667-295-42
; Sequence 42, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(141)
; OTHER INFORMATION: Ceres Seq. ID no. 6425769
US-10-667-295-42

Query Match 10.8%; Score 58; DB 6; Length 141;
Best Local Similarity 23.3%; Pred. No. 3.6;
Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps 2;

Qy 8 AVLRAIDGINQRSSDANLYRLDLLDPRPTMGDPTPKPVSFYKVTVCPRTTQOSPDC 67
Db 74 SVVGAVDGV-----AMEVDVDSAK-----TNSNSDK 101

RESULT 8
US-11-100-183-15
; Sequence 15, Application US/11100183
; Publication No. US2005027074A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene California
; TITLE OF INVENTION: Compositions And Methods For Reverse Transcription
; FILE REFERENCE: 25436/2452
; CURRENT APPLICATION NUMBER: US/11/100,183
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/559,810
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 15
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-100-183-15
```

```
; OTHER INFORMATION: Ceres Seq. ID no. 6425770
US-10-667-295-43

Query Match 10.8%; Score 58; DB 6; Length 102;
Best Local Similarity 23.3%; Pred. No. 2.4;
Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps 2;

Qy 8 AVLRAIDGINQRSSDANLYRLDLLDPRPTMGDPTPKPVSFYKVTVCPRTTQOSPDC 67
Db 35 SVVGAVDGV-----AMEVDVDSAK-----TNSNSDK 62

Qy 68 DFKDGLVKRCMGVTTLNQARGSPDI 93
Db 63 SEKDGRKRLCVGSQALNYRDRHMEI 88

RESULT 9
US-10-667-295-42
; Sequence 42, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(141)
; OTHER INFORMATION: Ceres Seq. ID no. 6425769
US-10-667-295-42

Query Match 10.8%; Score 58; DB 6; Length 141;
Best Local Similarity 23.3%; Pred. No. 3.6;
Matches 20; Conservative 10; Mismatches 24; Indels 32; Gaps 2;

Qy 8 AVLRAIDGINQRSSDANLYRLDLLDPRPTMGDPTPKPVSFYKVTVCPRTTQOSPDC 67
Db 74 SVVGAVDGV-----AMEVDVDSAK-----TNSNSDK 101

Qy 68 DFKDGLVKRCMGVTTLNQARGSPDI 93
Db 102 SEKDGRKRLCVGSQALNYRDRHMEI 127

RESULT 10
US-11-100-183-15
; Sequence 15, Application US/11100183
; Publication No. US2005027074A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene California
; TITLE OF INVENTION: Compositions And Methods For Reverse Transcription
; FILE REFERENCE: 25436/2452
; CURRENT APPLICATION NUMBER: US/11/100,183
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/559,810
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 15
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-11-100-183-15
```

Query Match	10.6%	Score 56.5;	DB 7;	Length 897;
Best Local Similarity	30.9%	Pred. No. 56;		
Matches 17;	Conservative	6;	Mismatches 23;	Indels 9;
Gaps 2;				

```

, GENERAL INFORMATION:
, APPLICANT: KIMMERLY, WILLIAM JOHN
, TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
, FILE REFERENCE: PU3480US
, CURRENT APPLICATION NUMBER: US/10/793,626
, CURRENT FILING DATE: 2004-03-04
, PRIOR APPLICATION NUMBER: 60/164,258
, PRIOR FILING DATE: 1999-11-09
, NUMBER OF SEQ ID NOS: 4472
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 566
, LENGTH: 244
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: synthetic
, OTHER INFORMATION: amino acid sequence
US-10-793-626-566

```

```

; ORGANISM: Homo sapiens
US-11-137-465-36

Query Match      10.6%   Score 56.5;   DB 7;   Length 993;
Best Local Similarity 30.9%;   Pred. No. 64;
Matches 17;   Conservative 6;   Mismatches 23;   Indels 9;   Gaps:

Qy      46  PVSFTVKETVCPRTTQSPBDCDFKDKGLVKRCMGTVTLNQARGSFDISCDKDNK 100
      ||| : : : : : ||| : : : : : ||| : : : : :
Db      263 PVGFMLQP---DRKTKDIDECLNNGGCDHICRNTV-----GSFECSCKKGYK 308

RESULT 12
US-11-113-424-37
; Sequence 37, Application US/1113424
; Publication NO. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424

```



```

; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 37
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-113-424-37

Query Match          10.6%; Score 56.5; DB 7; Length 997;
Best Local Similarity 30.9%; Pred. No. 64;
Matches 17; Conservative 6; Mismatches 23; Indels 9; Gaps 2;

Qy 46 PVSFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARSGPDISCDKNK 100
Db 307 PTGFTLQ---VDGKTKDIDCQTRNGCGNHFKNTV-----GSFDCSCKKGPK 352

RESULT 13
US-10-467-657-7834
; Sequence 7834, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7834
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7834

Query Match          10.5%; Score 56; DB 6; Length 118;
Best Local Similarity 29.7%; Pred. No. 5;
Matches 19; Conservative 7; Mismatches 18; Indels 20; Gaps 4;

Qy 21 SDANLYRLDLDPRMTDGP-----DTPKDVSTVKETVCPRTTQSPEDCDPKDGLV 75
Db 68 SSADLLRYRIQTAP-WFSEPPKTELDPKNVSFCSIGTNCP-----APSD----- 112

Qy 76 KRCM 79
Db 113 NRCL 116

Search completed: January 12, 2006, 21:54:25
Job time : 4.47232 secs
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RESULT 14
US-10-793-626-2964
; Sequence 2964, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800S
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2964
; LENGTH: 5024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5024)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2964

Query Match          10.5%; Score 56; DB 6; Length 5024;
Best Local Similarity 34.2%; Pred. No. 5.6e+02;
Matches 13; Conservative 7; Mismatches 12; Indels 6; Gaps 1;

Qy 6 KEAVLRAIDGINQRSSDANLYRLDLDPR-----PTM 37
Db 3196 KEIKQLTDAVQNQANDLNGVELLDADKQNAHQSIPTL 3233

RESULT 15
US-10-995-561-878
; Sequence 878, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 878
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-878

Query Match          10.4%; Score 55.5; DB 6; Length 729;
Best Local Similarity 23.5%; Pred. No. 57;
Matches 23; Conservative 16; Mismatches 30; Indels 29; Gaps 3;

Qy 2 VLSKEAVLRAIDGINQRSSDANLYRLDLDPRMTDGPDPDPKPVSTVKETVC----- 56
Db 363 LLGRKSELDAKD--SSSSNLSLKV-----RPSSDLNNSGTQSPHHKQVRSVSSQK 415

Qy 57 -----PRTTQSPEDCDPKDGLVKR 77
Db 416 RRYSDHAGPAIPSVVAYPKRSQTSTADSLKEDGISR 453

Search completed: January 12, 2006, 21:54:25
Job time : 4.47232 secs
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314

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:41:48 ; Search time 90.3321 Seconds
(without alignments)
826.886 Million cell updates/sec

Title: US-10-815-562-2
Perfect score: 879
Sequence: 1 MKTQDGHSLGRWSLVLLLL.....KRIQRIKDFLNLPRTES 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	100.0	170	3	AAB07901
2	879	100.0	170	7	ADf18219 Protein s
3	879	100.0	170	8	Adi29582 Human CAP
4	879	100.0	170	8	Adj82973 Human Pep
5	879	100.0	170	8	Adr47315 Human cat
6	879	100.0	170	9	Adw43827 Mouse che
7	875	99.5	169	9	Adk70797 Human CAP
8	874	99.4	170	2	Aar92924 Prepro-PA
9	874	99.4	170	2	Aau90996 Transplan
10	874	99.4	170	7	Adp65263 Human cat
11	874	99.4	170	8	Adn41827 Human Lu-
12	874	99.4	170	8	Abm80449 Tumour-as
13	874	99.4	170	9	ABN80449
14	874	99.4	170	9	Adx08374 Cathelici
15	865	98.4	170	5	Adz80363 Human cat
16	819	93.2	177	4	Abb07707 Human pep
17	761	86.6	152	3	Aau31061 Novel hum
18	730	83.0	140	8	Aag03781 Human sec
19	690	78.5	170	9	Adj82974 Human Pep
20	493.5	56.1	172	9	Aea00315 Human cat
21	468.5	53.3	171	5	Adz80366 Canine ca
22	457.5	52.0	170	5	Abb07703 Rabbit pe
23	457.5	52.0	170	5	Aau90997 Transplan
24	451	51.3	156	5	Adx08375 Myeloid c
					Aau90999 Transplan

25	451	51.3	156	9	ADX08377
26	442.5	50.3	176	9	Adz80368
27	433.5	49.3	173	9	Adz80365
28	432	49.1	159	5	Aau90998
29	432	49.1	159	9	ADX08376
30	431.5	49.1	173	5	ABB07701
31	427.5	48.6	155	5	ABB07704
32	427.5	48.6	155	5	Aau90993
33	427.5	48.6	155	9	ADX08371
34	424.5	48.3	149	2	AAW18157
35	421.5	48.0	172	9	ADZ80367
36	418.5	47.6	147	2	AAW18158
37	418.5	47.6	149	2	AAW25081
38	418.5	47.6	149	2	AAW18156
39	418.5	47.6	149	2	AAW09087
40	418.5	47.6	149	2	AAW18159
41	415.5	47.3	147	8	ADL18364
42	415.5	47.3	149	8	ADL18362
43	415.5	47.3	149	8	ADL18366
44	415.5	47.3	149	8	ADL18368
45	413	47.0	158	6	ABP70875

ALIGNMENTS

RESULT 1
AAB07901
ID AAB07901 standard; protein; 170 AA.
XX
AC AAB07901;
XX
DT 14-NOV-2000 (first entry)
XX
DE A human cationic protein designated CAP18.
XX
KW Human; cationic protein; lipopolysaccharide binding; anticoagulant;
KW CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis;
KW coagulation-related disorder; disseminated intravascular coagulation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 134..170
FT /note= "reactive nitrogen inhibitory protein"
XX
PN US6103888-A.
XX
PD 15-AUG-2000.

XX 01-JUN-1999; 99US-00322911.
XX 17-JUL-1992; 92US-00916761.
XX 17-JUL-1992; 92US-00916761.
XX 15-JUL-1993; 93WO-US0006731.
XX 27-SEP-1994; 94US-00313681.
XX 01-AUG-1996; 96US-00691280.
XX (PANO-) PANORAMA RES INC.
XX Larrick JW, Wright SC, Hirata M;
XX WPI; 2000-531989/48.
XX N-PSDB; AAA59574.
XX Novel human cDNA encoding cationic proteins having lipopolysaccharide
XX binding and anticoagulant activity, useful for treating and diagnosing
XX gram negative sepsis and disseminated intravascular coagulation.
XX Disclosure; Col 29-30; 46pp; English.
XX The present sequence represents a human cationic protein, having
XX lipopolysaccharide binding and anticoagulant activity. The polypeptide is

CC designated CAP18. Amino acids 134-170 of CAP18 represent a reactive
CC nitrogen inhibitory protein (RNIP). The CAP18 polynucleotide is useful
CC for producing cationic proteins. The CAP18 polypeptide is useful for
CC treating and diagnosing lipopolysaccharide-associated conditions such as
CC gram negative sepsis, and/or coagulation-related disorders, such as
CC disseminated intravascular coagulation
XX

XX Sequence 170 AA;

Query Match 100.0%; Score 879; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 4e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTORQDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
DB 1 MKTORQDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
QY 61 LDPRTMDGDDPTPKPVSTFKETVCPRTTQOSPEDCDFKKGVLKRCMGTVTLNQARGS 120
DB 61 LDPRTMDGDDPTPKPVSTFKETVCPRTTQOSPEDCDFKKGVLKRCMGTVTLNQARGS 120
QY 121 FDISCDKDKRFPALLGDPFRKSKGKFKRIVQRIKDFLNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDPFRKSKGKFKRIVQRIKDFLNLVPRTES 170

RESULT 2

ADFI8219
ID ADFI8219 standard; protein; 170 AA.

XX ADFI8219;

DT 12-FEB-2004 (first entry)

XX Protein sequence.

XX Antimicrobial; LL-37; hCAP-18; antiarteriosclerotic; antiulcer;
XX vulnerary; cytosstatic.

XX Unidentified.

XX Key Location/Qualifiers
FT Misc-difference 6 /note= "Encoded by AAT"

XX EPI358888-A1.

XX 05-NOV-2003.

XX 27-FEB-2003; 2003EP-00004306.

XX 28-FEB-2002; 2002EP-00004656.

XX (BALS/) BALS R.

XX (KOCZ/) KOCZULLA A R.

XX (VDEG/) VON DEGENFELD G.

XX Bals R, Koczulla AR, Von Degenfeld G;

XX WPI; 2003-879818/82.

XX N-PSDB; ADFI8220.

XX Use of a peptide LL-37 for the preparation of a composition for
PT preventing or treating wounds or a disease caused reduced blood flow,
PT e.g. atherosclerosis, coronary heart disease, stroke, arterial occlusive
PT diseases or ulcer.

XX Disclosure; Page; 15pp; English.

XX The present invention is based on the finding that human antimicrobial
CC peptide LL-37 ADFI8218 is capable of inducing functionally important
CC angiogenesis in cell culture and in vivo by activation of the receptor
CC molecule FPRL1. LL-37 can be used in the preparation of a pharmaceutical

CC composition for the prevention or treatment of a disease caused by, or
CC resulting in, a reduced level of angiogenesis or arteriogenesis, or for
CC the treatment of (infected) wounds or cancer. The disease may be
CC associated with reduced blood flow, such as atherosclerosis, coronary
CC heart disease, stroke, arterial occlusive disease or an ulcer.
CC Suppression of angiogenesis through inhibition of LL-37 can be used to
CC treat tumours, especially a carcinoma or sarcoma including cancer of the
CC bile duct, brain, breast, colon, stomach, male and female reproductive
CC organs, lung and airways, skin, gallbladder, liver, nasopharynx, nerve
CC cells, kidney, prostate, and Kaposi's sarcoma (all claimed). The present
CC protein sequence is not explained in the specification.

XX Sequence 170 AA;

Query Match 100.0%; Score 879; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 4e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTORQDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
DB 1 MKTORQDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60

QY 61 LDPRTMDGDDPTPKPVSTFKETVCPRTTQOSPEDCDFKKGVLKRCMGTVTLNQARGS 120
DB 61 LDPRTMDGDDPTPKPVSTFKETVCPRTTQOSPEDCDFKKGVLKRCMGTVTLNQARGS 120

QY 121 FDISCDKDKRFPALLGDPFRKSKGKFKRIVQRIKDFLNLVPRTES 170

DB 121 FDISCDKDKRFPALLGDPFRKSKGKFKRIVQRIKDFLNLVPRTES 170

RESULT 3

ADI29582
ID ADI29582 standard; protein; 170 AA.

XX ADI29582;

DT 22-APR-2004 (first entry)

XX Human CAP18, SEQ ID 4.

XX CAP18; cationic antimicrobial protein of 18 kDa; bacterial pneumonia;
XX chronic lung disease; acute lung disease; inflammatory lung disease;
XX ARDS; bronchial asthma; human.

XX Homo sapiens.

XX WO2004009640-A1.

XX 29-JAN-2004.

XX 22-JUL-2003; 2003WO-JP009267.

XX 22-JUL-2002; 2002JP-00213040.

XX 14-MAR-2003; 2003JP-00070932.

XX (SEBK) SEIKAGAKU CORP.

XX Kirikae T, Toyooka K, Naiki Y, Tamura H, Ishizaka A, Hashimoto S;

XX WPI; 2004-143269/14.

XX New antibody against an antibacterial peptide, particularly human CAP18,
PT applicable in reagents and kits for detection, diagnosis and monitoring
PT of bacterial pneumonia.

XX Disclosure; SEQ ID NO 4; 52pp; Japanese.

XX The present invention relates to a novel CAP18 (cationic antimicrobial
CC protein of 18 kDa) antibody that can bind with human CAP18 peptide
CC fragments ADI29579-ADI29581. The antibody is useful in reagents and kits
CC for the detection, diagnosis and monitoring bacterial pneumonia and other
CC CAP18-related diseases like chronic and acute lung diseases, inflammatory

CC lung diseases, ARDS and bronchial asthma. The present sequence is human
 CC CAP18.
 CC
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 879; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 Db 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKQDGLVKRCMGTVTLLNQARGS 120
 Db 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKQDGLVKRCMGTVTLLNQARGS 120
 QY 121 FDISCDKDKNRPALLGDFPKSKKEKIGKEFKRIVQRIKDFLNLVPTES 170
 Db 121 FDISCDKDKNRPALLGDFPKSKKEKIGKEFKRIVQRIKDFLNLVPTES 170
 RESULT 4
 ADJ82973
 ID ADJ82973 standard; protein; 170 AA.
 AC ADJ82973;
 DT 06-MAY-2004 (first entry)
 XX Human Pep714-related peptide precursor SEQ ID NO: 1.
 DE pep714-related peptide; precursor; human; secreted peptide; Pep714;
 KW oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
 KW pneumonia.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..30 /label= signal_peptide
 FT Protein 31..131 /label= propeptide
 FT Cleavage-site 106..107 /note= "dibasic peptidase cleavage site"
 FT Cleavage-site 130..131 /note= "dibasic peptidase cleavage site"
 FT Protein 132..170 /note= "dibasic peptidase cleavage site"
 FT Protein 134..170 /label= antibacterial_protein_FALL-39
 FT Cleavage-site 140..141 /label= antibacterial_protein_LL-37
 FT Cleavage-site 151..152 /note= "dibasic peptidase cleavage site"
 FT Cleavage-site 151..152 /note= "dibasic peptidase cleavage site"
 XX WO2004005338-A1.
 XX 15-JAN-2004.
 XX 30-JUN-2003; 2003WO-EP006930.
 XX 08-JUL-2002; 2002US-0394486P.
 PR 07-JUN-2003; 2003US-0438602P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Jeandenans C, Niknejad A;
 XX

DR WPI; 2004-099371/10.
 XX Novel Pep714-related polypeptide having biological activity, useful for
 PT treatment and prevention of microbial or viral infection, cystic fibrosis
 PT and chronic respiratory infections.
 XX Disclosure; Page 91-92; 99pp; English.
 XX The present invention relates to a Pep714-related peptide. This is useful
 CC for inhibiting microbial propagation, preferably viral propagation, and
 CC in the treatment of chemotherapy and radiotherapy induced oral mucositis,
 CC oral lesion, ventilator associated pneumonia, chronic respiratory
 CC infections and cystic fibrosis. The present sequence is a Pep714-related
 CC peptide precursor protein shown in the exemplification of the invention.
 XX Sequence 170 AA;
 SQ
 Query Match 100.0%; Score 879; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 Db 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKQDGLVKRCMGTVTLLNQARGS 120
 Db 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKQDGLVKRCMGTVTLLNQARGS 120
 QY 121 FDISCDKDKNRPALLGDFPKSKKEKIGKEFKRIVQRIKDFLNLVPTES 170
 Db 121 FDISCDKDKNRPALLGDFPKSKKEKIGKEFKRIVQRIKDFLNLVPTES 170
 RESULT 5
 ADJ47315
 ID ADJ47315 standard; protein; 170 AA.
 AC ADJ47315;
 DT 18-NOV-2004 (first entry)
 XX Human cationic antimicrobial protein-18.
 DE Human cationic antimicrobial protein-18.
 KW cystic pulmonary fibrosis; cationic antimicrobial protein; CAP18;
 KW pulmonary disease.
 XX Homo sapiens.
 XX JP2004245842-A.
 PN 02-SEP-2004.
 PD 13-FEB-2004; 2004JP-00036471.
 PF 14-FEB-2003; 2003US-047310P.
 PR (SEK) SEIKAGAKU KOGYO CO LTD.
 PA WPI; 2004-629858/61.
 XX Evaluating cystic pulmonary fibrosis, by measuring cationic antimicrobial
 PT protein of 18 kDa (CAP18) quantity in biological sample, and evaluating
 PT fibrosis by comparing measured quantity and quantity of CAP18 in control
 PT sample.
 XX Disclosure; SEQ ID NO 4; 14pp; Japanese.
 XX The invention relates to a novel method for evaluating cystic pulmonary
 CC fibrosis. The method comprises: measuring the quantity of cationic
 CC antimicrobial protein of 18 kDa (CAP18) in the biological sample
 CC collected from the individual; comparing the quantity of CAP18 measured
 CC in the previous step and the quantity of CAP18 in a control sample; and
 CC

CC evaluating cystic pulmonary fibrosis by associating comparison of
 CC obtained results. The invention further comprises: a kit for carrying out
 CC the evaluating method, comprising a solid-phase component and an antibody
 CC coupled with an antigenic peptide having a sequence of ABR47312, or a
 CC solid-phase component comprising an immobilised antibody (first antibody)
 CC which is coupled with the antigenic peptide, and the antibody (second
 CC antibody) coupled with the antigenic peptide. The method or kit are
 CC useful for evaluating cystic pulmonary fibrosis in an individual, where
 CC the evaluation includes diagnosis for the presence or absence of a risk
 CC of cystic pulmonary fibrosis, evaluation of serious or acute conditions,
 CC or the evaluation of the advanced grade of the disease. The method
 CC enables simple, cost-effective, rapid, highly sensitive and highly
 CC accurate evaluation of the acute or serious conditions, or the
 CC advancement of the pulmonary diseases. This sequence represents the human
 CC CAP18 protein of the invention.

XX Sequence 170 AA;
 CC Query Match 100.0%; Score 879; DB 8; Length 170;
 CC Best Local Similarity 100.0%; Pred. No. 4e-89;
 CC Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTQRDGHSLGRWSLVLLLLGLVMPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 DB 1 MKTQRDGHSLGRWSLVLLLLGLVMPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKGVLKRCMGTVTLNQARGS 120
 DB 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKGVLKRCMGTVTLNQARGS 120
 QY 121 FDISCDKDKRKFALLGDFPRKSKKEIGKEFKRIVQRIKDFLRNLVPRTES 170
 DB 121 FDISCDKDKRKFALLGDFPRKSKKEIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 6
 ADW43827
 ID ADW43827 standard; peptide; 170 AA.
 XX AC ADW43827;
 XX DT 24-MAR-2005 (first entry)
 XX Mouse chemerin peptide SEQ ID NO 51.
 DE gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cna-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.
 XX Mus musculus.
 OS WO200500875-A2.
 FN 06-JAN-2005.
 PD 25-JUN-2004; 2004WO-EP006945.
 PP 25-JUN-2003; 2003US-00603566.
 XX (EURO-) EUROSREEN SA.
 XX Wittamer V, Communi D, Dethoux M, Parmentier M, Loison C;
 FI Ooms FDR;
 XX WPI; 2005-058121/06.
 XX New Chemerin polypeptides, useful for diagnosing and treating a disease,
 PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura,
 PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
 PT Disease, or histiocytosis.

PS Example 2; SEQ ID NO 51; 183bp; English.
 XX The invention describes a polypeptide (I) of up to 50 amino acids where
 CC the polypeptide binds specifically to a chemerin polypeptide. Also
 CC described are: a nucleic acid sequence encoding (I); an expression vector
 CC comprising the coding sequence of the nucleic acid; a transgenic animal
 CC transfecting with the expression vector; a (therapeutic) composition
 CC comprising (I) and an isolated Chemerin polypeptide or a nucleic acid
 CC sequence of (I); an antibody that selectively binds to (I); identifying
 CC an agent that modulates the interaction between a Chemerin polypeptide
 CC and a Chemerin polypeptide; detecting the presence, in a sample, of an
 CC agent that modulates the interaction between a Chemerin polypeptide and a
 CC Chemerin polypeptide in a sample; identifying an agent that modulates
 CC the function of Chemerin polypeptide; detecting the presence, in a
 CC sample, of an agent that modulates the function of Chemerin polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC Chemerin (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of Chemerin polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC Chemerin polypeptide signaling, comprising an isolated Chemerin
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transformed with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a Chemerin polynucleotide
 CC encoding (I); identifying an antibody inhibiting Chemerin activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's
 CC Macroglobulinemia, Gaucher's disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a mouse chemerin peptide used to analyse
 CC processing of immature chemerin.

XX Sequence 170 AA;
 CC Query Match 100.0%; Score 879; DB 9; Length 170;
 CC Best Local Similarity 100.0%; Pred. No. 4e-89;
 CC Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTQRDGHSLGRWSLVLLLLGLVMPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 DB 1 MKTQRDGHSLGRWSLVLLLLGLVMPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKGVLKRCMGTVTLNQARGS 120
 DB 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKKGVLKRCMGTVTLNQARGS 120
 QY 121 FDISCDKDKRKFALLGDFPRKSKKEIGKEFKRIVQRIKDFLRNLVPRTES 170
 DB 121 FDISCDKDKRKFALLGDFPRKSKKEIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 7
 ADK70797
 ID ADK70797 standard; protein; 169 AA.
 XX AC ADK70797;
 XX DT 06-MAY-2004 (first entry)
 XX Human CAP18 full-length protein.
 DE alpha-helix; thionine; antibacterial; antifungal; plant;
 KW fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
 KW Pseudomonas; antimicrobial; rabbit; CAP18.
 OS Homo sapiens.
 XX JP2003204794-A.

XX PD 22-JUL-2003.
XX PF 15-JAN-2002; 2002JP-00006607.
XX PR 15-JAN-2002; 2002JP-00006607.
XX PA (TOYW) TOYOTA CHUO KENKYUSHO KK.
XX WPI; 2004-102620/11.
XX Antimicrobial polypeptide composition for a plant pathogen, comprises one or more types of thionine and/or a polypeptide having an alpha helix structure, as an active ingredient.
XX Disclosure; SEQ ID NO 38; 27pp; Japanese.
XX The invention relates to a novel polypeptide composition for preventing disease in an organism which comprises one or more types of polypeptide which have an alpha-helix structure and/or thionine component. The composition of the invention demonstrates antibacterial and antifungal activities and may be useful for preventing a disease in an organism, for generating cultivated plants and in providing resistance to plant tissue against fungi such as *Pyricularia oryzae* (rice blast fungus), *Ceratomyces fimbriata* and bacteria such as *Pseudomonas* etc. The composition has high antimicrobial activity at low concentration. The current sequence is that of the rabbit CAP18 full-length protein of the invention.
XX SQ Sequence 169 AA;
Query Match 99.5%; Score 875; DB 8; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.1e-88;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
DB 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
QY 61 LDPRFTMDGDDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 120
DB 61 LDPRFTMDGDDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 120
QY 121 FDISCDKNKRPALLGDFFRKSKEKIGKEFKRIVQRIKDFLNLYPRTES 169
DB 121 FDISCDKNKRPALLGDFFRKSKEKIGKEFKRIVQRIKDFLNLYPRTES 169
RESULT 8
AAR92924
ID AAR92924 standard; protein; 170 AA.
XX AC AAR92924;
XX DT 06-JUN-1996 (first entry)
XX DE Prepro-FALL-99.
XX KW FALL-39; cathelin; antibiotic; antimicrobial; antibacterial.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..131
XX FT Protein /label= Prepro-peptide
XX FT Protein 132..170
XX FT Protein /label= FALL-39
XX PN WO9608508-A1.
XX PD 21-MAR-1996.
XX PF 12-SEP-1995; 95WO-S0001030.

XX PR 13-SEP-1994; 94SE-00003055.
XX PA (BOMA/) BOWAN H G.
XX PI Agerberth B, Gudmundsson GH, Gunne H;
XX WPI; 1996-179899/18.
XX N-PSDB; AAT18233.
XX Novel peptide antibiotic, FALL-39 - overcomes classical antibiotic resistance and is non-cytotoxic.
XX Example 2; Fig 1; 26pp; English.
XX Novel cathelin-like prepro-FALL-39 (AAR92924) is the precursor of the antimicrobial, antibacterial agent FALL-39 (see AAR92923). It is the product of a cDNA clone (AAT18233) isolated from a human bone marrow cDNA library. FALL-39 includes a helical region (see AAR92922) that is required for biological activity. FALL-39 is useful therapeutically for inhibiting microbial growth in mammals, including humans, and is non-cytotoxic
XX SQ Sequence 170 AA;
Query Match 99.4%; Score 874; DB 2; Length 170;
Best Local Similarity 99.4%; Pred. No. 1.4e-88;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
DB 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
QY 61 LDPRFTMDGDDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 120
DB 61 LDPRFTMDGDDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 120
QY 121 FDISCDKNKRPALLGDFFRKSKEKIGKEFKRIVQRIKDFLNLYPRTES 170
DB 121 FDISCDKNKRPALLGDFFRKSKEKIGKEFKRIVQRIKDFLNLYPRTES 170
RESULT 9
AAU90996
ID AAU90996 standard; peptide; 170 AA.
XX AC AAU90996;
XX DT 05-JUN-2002 (first entry)
XX DE Transplant media associated antimicrobial peptide #32.
XX KW Transplant; antimicrobial peptide; pore forming agent;
XX KW cell surface receptor binding compound; kidney transplant; cardioplegia;
XX KW organ transplant; transplant rejection.
XX OS Homo sapiens.
XX PN WO200209738-A1.
XX PD 07-FEB-2002.
XX PF 27-JUL-2001; 2001WO-US023785.
XX PR 28-JUL-2000; 2000US-0221632P.
XX PR 17-NOV-2000; 2000US-0249602P.
XX PR 15-MAY-2001; 2001US-0290932P.
XX PA (MURP/) MURPHY C J.
XX PI Murphy CJ, Reid TW, Mcanulty JF;
XX DR WPI; 2002-268995/31.

XX Media comprising antimicrobial polypeptides or pore forming agents and/or
PT cell surface receptor binding compounds useful for the storage and
PT preservation of organs prior to transplant.
XX
XX Disclosure; Page 27; 78pp; English.
XX
XX The invention describes new transplant compositions comprising
XX antimicrobial polypeptides or pore forming agents and/or cell surface
XX receptor binding compounds. The media is capable of extending the
XX preservation period past 72 hours and can provide organs with increased
XX functionality upon transplant. Animals receiving kidneys stored in the
XX media of the present invention for either three or four days had serum
XX creatinine levels of less than half of those observed in control animals
XX receiving kidneys stored in UW solution (defined in the specification)
XX alone. Lower serum creatinine levels are indicative of healthier kidneys
XX and a more preferable prognosis for the transplant patient. The media of
XX the invention are useful for decreasing the incidence and/or severity of
XX delayed graft function in patients receiving transplanted kidneys stored
XX and/or treated in the media. The media may also be used in procedures
XX such as cardioplegia. It is contemplated that transplant of healthier
XX organs leads to a decrease in chronic rejection. This sequence represents
XX an antimicrobial peptide studied in the development of the transplant
XX media
SQ Sequence 170 AA;
Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 1.4e-88;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTORHGSLGRWSLVLLGLVMPALIAQVLSYKEAVLRADGINORSSDANLYRLLD 60
DB 1 MKTORHGSLGRWSLVLLGLVMPALIAQVLSYKEAVLRADGINORSSDANLYRLLD 60
QY 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQSPEDCDFKDGKLVKRCMGTVTLNQARGS 120
DB 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQSPEDCDFKDGKLVKRCMGTVTLNQARGS 120
QY 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKPKRIVQRIKDFLRNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKPKRIVQRIKDFLRNLVPRTES 170
RESULT 10
ADP65263
ID ADP65263 standard; protein; 170 AA.
XX
XX ADP65263;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human cathelicidin antimicrobial peptide.
XX
XX autoimmune disease; arthritis; gene expression analysis;
XX rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
XX antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
XX immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
XX fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
XX immune; human.
XX
XX Homo sapiens.
XX
XX WO2003072827-A1.
XX
XX 04-SEP-2003.
XX
XX 31-OCT-2002; 2002WO-US035433.
XX
XX 31-OCT-2001; 2001US-0336220P.
XX
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX

PI Hirsch R, Thorton SL;
XX WPI; 2003-712740/67.
DR GENBANK, NP_004336.
XX
XX Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
XX Disclosure; Page; 56pp; English.
XX
XX The invention relates to a novel method for diagnosing and analysing
XX autoimmune disease or arthritides. The method comprises obtaining a
XX patient sample containing mRNA, analysing gene expression using the mRNA
XX that results in a gene expression signature of the mRNA, and using that
XX gene expression signature to diagnose or analyse the autoimmune disease
XX or arthritides in the patient, where gene expression of at least 60% of
XX the genes correlates with that of the gene signature. The invention
XX further comprises: a treatment of rheumatoid arthritis; identification of
XX genes for targeting in the treatment of rheumatoid arthritis in a mammal
XX other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
XX array or gene chip, specific for rheumatoid arthritis; diagnosis or
XX analyses of autoimmune disease or rheumatoid arthritis; screening the
XX efficacy of a candidate drug in vitro for the treatment of collagen-
XX induced arthritis; and reducing the symptoms associated with collagen-
XX induced arthritis. The compositions of the invention have the following
XX activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
XX antigout, antiinflammatory, dermatological, and immunomodulatory. The
XX methods and compositions of the present invention are useful for
XX diagnosing and treating autoimmune disease or arthritides, such as
XX rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
XX fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
XX immune disease caused by an infectious agent. This sequence represents a
XX protein sequence relating to the genes used in the analysis and treatment
XX of autoimmune diseases or arthritides. Note: This sequence is not shown
XX in the specification. It has been supplied in an electronic format from
XX WIPO.
SQ Sequence 170 AA;
Query Match 99.4%; Score 874; DB 7; Length 170;
Best Local Similarity 99.4%; Pred. No. 1.4e-88;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTORHGSLGRWSLVLLGLVMPALIAQVLSYKEAVLRADGINORSSDANLYRLLD 60
DB 1 MKTORHGSLGRWSLVLLGLVMPALIAQVLSYKEAVLRADGINORSSDANLYRLLD 60
QY 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQSPEDCDFKDGKLVKRCMGTVTLNQARGS 120
DB 61 LDPRTMDGDDPTPKPVSFTVKETVCPRTTQSPEDCDFKDGKLVKRCMGTVTLNQARGS 120
QY 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKPKRIVQRIKDFLRNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKPKRIVQRIKDFLRNLVPRTES 170
RESULT 11
ADN41827
ID ADN41827 standard; protein; 170 AA.
XX
XX ADN41827;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human LL-37 protein SEQ ID NO:2.
XX
XX infection; cathelicidin type peptide; LL-37; antimicrobial;
XX antiinflammatory; immunostimulant; bacterial infection; neutropenia;
XX toothpaste; mouthwash; gingivitis; oral infection; periodontitis; human.
XX
XX Homo sapiens.
XX

XX WO2004034061-A2.
 XX 22-APR-2004.
 XX 10-OCT-2003; 2003WO-EP011240.
 XX 10-OCT-2002; 2002GB-00023655.
 XX (MABT-) MABTECH AB.
 XX Boman H, Andersson M, Puetssep K, Carlsson G;
 XX WPI; 2004-364936/34.
 XX N-PSDB; ADN41826.
 XX Determination of susceptibility of subject to infection comprising
 XX detecting cathelicidin type peptide present in sample, optionally
 XX comparing level of peptide in sample to control sample.
 XX Disclosure; SEQ ID NO 2; 40pp; English.
 XX The present invention describes a method for determining the
 XX susceptibility of a subject to infection. The method comprises: (i)
 XX providing a sample from a subject; (ii) detecting any cathelicidin type
 XX peptide (LL-37) present in the sample; (iii) optionally comparing the
 XX level of LL-37 in the sample to a control sample; (iv) determining the
 XX susceptibility of the subject to infection (where no LL-37 or a low level
 XX of LL-37 indicates that subject is susceptible to infection); and (v)
 XX optionally administering an antimicrobial agent to reduce infection. Also
 XX described is a product containing LL-37 and a cytostatic drug,
 XX corticosteroid or growth factor (preferably recombinant granulocyte
 XX colony stimulating factor (G-CSF) or GM-CSF). The product has
 XX antimicrobial, antiinflammatory and immunostimulant activities. The
 XX method can be used for determining the susceptibility of a subject to
 XX infection such as bacterial infection (e.g. Actinobacillus
 XX actinomycetemcomitans infection) and neutropenia, and for diagnosing
 XX neutropenia (e.g. Kostmann morbus). The method is also useful in the
 XX manufacture of a medicament in the form of toothpaste or mouthwash for
 XX the preventative treatment of infection e.g. gingivitis, oral infection
 XX (such as periodontitis), and for the treatment of neutropenia. The method
 XX controls the normal flora in neutropenia and so combat infections. The
 XX present sequence represents the proform of human LL-37, which is used in
 XX the exemplification of the present invention.
 XX Sequence 170 AA;
 XX Query Match 99.4%; Score 874; DB 8; Length 170;
 XX Best Local Similarity 99.4%; Pred. No. 1.4e-88;
 XX Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTORHGSLGRWSLVLLLLGLVMPALIIAQLVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 Db 1 MKTORHGSLGRWSLVLLLLGLVMPALIIAQLVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120
 Db 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120
 QY 121 FDISCDKDKNGKRFALLGDFFRKSKKEKIGKFKRIVQRIKDFLRLNLPRTES 170
 Db 121 FDISCDKDKNGKRFALLGDFFRKSKKEKIGKFKRIVQRIKDFLRLNLPRTES 170
 RESULT 12
 ABM80449
 ID ABM80449 standard; protein; 170 AA.
 XX
 XX ABM80449;
 AC
 XX
 XX 18-NOV-2004 (first entry)
 DT
 XX Tumour-associated antigenic target (TAT) polypeptide PRO36373, SEQ:1129.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.
 XX Homo sapiens.
 OS
 XX WO2004030615-A2.
 PN
 XX 15-APR-2004.
 PD
 XX 29-SEP-2003; 2003WO-US028547.
 PF
 XX 02-OCT-2002; 2002US-0414971P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Wu TD, Zhang Z, Zhou Y;
 FI
 XX WPI; 2004-347921/32.
 XX N-PSDB; ACN37923.
 DR
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 XX useful in preparing a medicament for treating or detecting a
 XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 XX prostate cancer or tumor.
 PT
 XX Claim 12; SEQ ID NO 1129; 7273pp; English.
 PS
 XX The invention relates to human tumour-associated antigenic target (TAT)
 XX polypeptides, and their related nucleic acids. The TAT polypeptides are
 XX overexpressed in cancer tissues compared to normal tissues, and may thus
 XX serve as effective targets for the diagnosis and treatment of cancer in
 XX mammals. The invention also relates to nucleic acid and polypeptide
 XX sequences at least 80% identical to the TAT nucleic acids and
 XX polypeptides; expression vectors and host cells comprising a TAT nucleic
 XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
 XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
 XX TAT polypeptide; and methods and compositions for the treatment or
 XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 XX antibodies, antagonists, binding molecules and compositions are useful
 XX for diagnosing or treating a cell proliferative disorder associated with
 XX increased TAT expression, particularly cancers such as breast cancer,
 XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 XX cancer, pancreatic cancer, cervical cancer, cancers of the central
 XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 XX used as hybridisation probes, in chromosome and gene mapping, in
 XX chromosome identification and in gene therapy. The present sequence
 XX represents a TAT polypeptide of the invention
 XX Sequence 170 AA;
 XX Query Match 99.4%; Score 874; DB 8; Length 170;
 XX Best Local Similarity 99.4%; Pred. No. 1.4e-88;
 XX Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTORHGSLGRWSLVLLLLGLVMPALIIAQLVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 Db 1 MKTORHGSLGRWSLVLLLLGLVMPALIIAQLVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 QY 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120
 Db 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGVTTLNQARGS 120
 QY 121 FDISCDKDKNGKRFALLGDFFRKSKKEKIGKFKRIVQRIKDFLRLNLPRTES 170
 Db 121 FDISCDKDKNGKRFALLGDFFRKSKKEKIGKFKRIVQRIKDFLRLNLPRTES 170

Query Match	99.4%;	Score 874;	DB 9;	Length 170;
Best Local Similarity	99.4%;	Pred. No. 1.4e-88;		
Matches 169;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MKTORGHISGRWSLVLLLLGLVMPALIAQAOLVLSYKEAVLRAIDGINORSSDANLYELLD	60
Db	1	MKTORGHISGRWSLVLLLLGLVMPALIAQAOLVLSYKEAVLRAIDGINORSSDANLYELLD	60
QY	61	LDRPRTMDGDPDPFKPVSFTVKETVCPRTTQQSPEDCDPKKDGVLVRCMGTVTTLNQARGS	120
Db	61	LDRPRTMDGDPDPFKPVSFTVKETVCPRTTQQSPEDCDPKKDGVLVRCMGTVTTLNQARGS	120
QY	121	FDISCDKNKRFPALLGDGDFRKSKEKIGKSPKRIVQRIKDFLRNLVPRTES	170
Db	121	FDISCDKNKRFPALLGDGDFRKSKEKIGKSPKRIVQRIKDFLRNLVPRTES	170

RESULT 14	
ADZ80363	
ID	ADZ80363 standard; protein; 170 AA.
XX	ADZ80363;
XX	AC
XX	DT
XX	14-JUL-2005 (first entry)
XX	Human cathelicidin polypeptide.
XX	
KW	Infection; viral infection; cathelicidin; atopic dermatitis;
KW	antimicrobial; virucide; dermatological; dermatological disease;
KW	immune disorder; inflammation.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Misc-difference 6
FT	/note= "Encoded by GAT"
XX	
XX	WO2005040201-A1.
XX	
PD	06-MAY-2005.
XX	
XX	20-OCT-2004; 2004WO-US034948.
XX	
XX	21-OCT-2003; 2003US-0512953P.
XX	
PA	(REGC) UNIV CALIFORNIA.
PA	(NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX	
PI	Gallo R, Murakami M, Leung DYM;
XX	
XX	WPI; 2005-355820/36.
DR	N-PADB; ADZ80362.
XX	
XX	Inhibiting spread and/or reducing risk of infection of virus, involves
PT	contacting virus with cathelicidin functional fragment.
XX	
PS	Disclosure; SEQ ID NO 6; 78pp; English.
XX	
CC	The invention relates to a method of inhibiting the spread and/or
CC	reducing the risk of infection of a virus, involving contacting a virus
CC	with a cathelicidin functional fragment. The invention also relates to a
CC	method of treating atopic dermatitis involving contacting a subject
CC	having or suspected of having atopic dermatitis with an inhibiting
CC	effective amount of a cathelicidin functional fragment. The cathelicidin
CC	functional fragment comprises a peptide with antimicrobial and/or
CC	antiviral activity. The methods are useful for inhibiting the spread
CC	and/or reducing the risk of infection of a virus and for treating atopic
CC	dermatitis. This sequence represents the human cathelicidin polypeptide
CC	of the invention.
XX	
XX	Sequence 170 AA;

Query Match 99.4%; Score 874; DB 9; Length 170;
 Best Local Similarity 99.4%; Pred. No. 1.4e-88;
 Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIQAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 DB 1 MKTQDGHSLGRWSLVLLGLVMPPLAIQAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60

QY 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNOARGS 120
 DB 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNOARGS 120

QY 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKFKRIVQRIKDFLNLVPTRES 170
 DB 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKFKRIVQRIKDFLNLVPTRES 170

RESULT 15
 ABB07707
 ID ABB07707 standard; peptide; 170 AA.
 AC ABB07707;
 DT 10-JUN-2002 (first entry)
 DE Human peptide antibiotic FALL-39 precursor sequence.
 XX Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
 KW antigen presenting cell; adjuvant; human; antibiotic; FALL-39.
 XX Homo sapiens.
 OS
 XX
 FN WO200213857-A2.
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-EP009529.
 XX
 PR 17-AUG-2000; 2000AT-00001416.
 XX
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX
 PI Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
 XX
 DR WPI; 2002-269154/31.
 XX
 PT Vaccine for active immunization or for preparing an adjuvant for
 PT enhancing an immune response to at least one antigen, comprises at least
 PT one antigen and at least one cathelicidin derived antimicrobial peptide.
 PS
 XX Disclosure; Fig 1; 65pp; English.
 XX
 CC The invention relates to a vaccine comprising at least one antigen and at
 CC least one cathelicidin derived antimicrobial peptide or its derivative.
 CC The vaccine is useful for active immunization, especially of humans or
 CC animals without protection against the specific antigen. The cathelicidin
 CC derived antimicrobial peptide is useful in the preparation of an adjuvant
 CC for enhancing the immune response to at least one antigen, where the
 CC adjuvant enhances the uptake of at least one antigen in antigen
 CC presenting cells (APC), and the adjuvant is added to the vaccine.
 CC Sequences ABB07701-07 represent cathelicidin proteins form various
 CC species
 XX
 SQ Sequence 170 AA;

Query Match 98.4%; Score 865; DB 5; Length 170;
 Best Local Similarity 98.8%; Pred. No. 1.4e-87;
 Matches 168; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTQDGHSLGRWSLVLLGLVMPPLAIQAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 DB 1 MKTQDGHSLGRWSLVLLGLVMPPLAIQAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60

QY 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNOARGS 120
 DB 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDPKDGLVKRCMGTVTLNOARGS 120

QY 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKFKRIVQRIKDFLNLVPTRES 170
 DB 121 FDISCDKDKRFPALLGDFPRKSKKEKIGKFKRIVQRIKDFLNLVPTRES 170

Search completed: January 12, 2006, 21:48:09
 Job time : 92.3321 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:43:14 ; Search time 15.0554 Seconds
(without alignments)
1086.448 Million cell updates/sec

Title: US-10-815-562-2

Perfect score: 879

Sequence: 1 MKTQRDGHSLGRWSLVLLLL.....KRIVQRIKDFLNLVPRTES 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	879	100.0	170	2 138932	CAP18 precursor -
2	874	99.4	170	2 S74248	antibacterial pept
3	465.5	53.0	171	2 J01171	18K lipopolysaccha
4	444.5	50.6	167	2 S88967	antibacterial pept
5	443.5	50.5	166	2 S41731	antibacterial prot
6	438.5	49.9	153	2 A53421	antibacterial pept
7	432.5	49.2	155	2 S68229	antimicrobial pept
8	431.5	49.1	173	2 S70521	cathelin-related p
9	429.5	48.9	228	2 S40463	prophenin (PP-2) p
10	427.5	48.6	155	2 S27018	bactenecin precurs
11	427.5	48.6	172	2 S68232	antimicrobial prot
12	424.5	48.3	149	2 S57609	protegrin 5 precu
13	418.5	47.6	147	2 JN0900	protegrin 2 precu
14	418.5	47.6	149	2 A53895	protegrin 3 precu
15	418.5	47.6	149	2 S57607	protegrin 1 precu
16	418.5	47.6	149	2 B53895	protegrin 4 precu
17	410.5	46.7	176	2 A45328	bactenecin 5 precu
18	406	46.2	160	2 S68412	indolicidin precu
19	405.5	46.1	144	1 J01222	indolicidin precu
20	399	45.4	160	2 S68228	myeloid antimicrob
21	396	45.1	152	2 S68411	cathelin-related p
22	387.5	44.1	212	2 S7330	cathelin-like anti
23	374.5	42.6	190	2 S68230	antimicrobial pept
24	319	36.3	96	1 XKPGC	cathelin - pig
25	172.5	19.6	135	2 B46634	polymorphonuclear
26	171.5	19.5	137	2 A46634	secreted phosphopr
27	85.5	9.7	200	2 I46051	kininogen, LMW II
28	85	9.7	434	1 KGBOL2	kininogen, LMW II
29	85	9.7	619	1 KGBOL2	kininogen, LMW II

30 84 9.6 436 1 KGBOL1 kininogen, LMW I p
31 84 9.6 621 1 KGBOL1 kininogen, LMW I p
32 82.5 9.4 273 2 AC1435 hypothetical prote
33 82 9.3 211 2 G01654 spp-24 precursor -
34 79 9.0 263 2 C84397 hypothetical prote
35 79 9.0 923 2 A53054 lipoxigenase (EC 1
36 78.5 8.9 445 2 T50802 serine/threonine p
37 78.5 8.9 1082 2 T31112 ATPase 2 (EC 3.6.1
38 77.5 8.8 444 2 T18804 hypothetical prote
39 77 8.8 518 2 S44637 F22b7.6 protein -
40 77 8.8 532 2 H84123 CTP synthetase ctr
41 77 8.8 2911 2 T20566 hypothetical prote
42 76.5 8.7 245 2 F84680 hypothetical prote
43 75 8.5 505 2 F95345 FixL Oxygen regula
44 75 8.5 505 2 S39984 nitrogen fixation
45 75 8.5 1599 2 T15854 hypothetical prote

ALIGNMENTS

RESULT 1

I38932

CAP18 precursor - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C:Accession: I38932

R:Larick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.

Infect. Immun. 63, 1291-1297, 1995

A:Title: Human CAP18: a novel antimicrobial lipopolysaccharide-binding protein.

A:Reference number: I38932; MUID:95197251; PMID:7890387

A:Accession: I38932

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-170 <RES>

A:Cross-references: UNIPROT:P49913; UNIPARC:UPI0000000A67; EMBL:U19970; NID:G643476; PID

A:Superfamily: cathelin; cystatin homology

F:22-130/Domain: cystatin homology <CYS>

Query Match 100.0%; Score 879; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.8e-77;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDPRPTWDGDDPTPKPVSTFKETVCPRTTQOSPEDCDPKDGLVKRCMGTTVLNQARGS 120
Db 61 LDPRPTWDGDDPTPKPVSTFKETVCPRTTQOSPEDCDPKDGLVKRCMGTTVLNQARGS 120
Qy 121 FDISCDKDKRKFALLGDFPFRRSKKEKIGKEFKRIQRIKDFLNLVPRTES 170
Db 121 FDISCDKDKRKFALLGDFPFRRSKKEKIGKEFKRIQRIKDFLNLVPRTES 170

RESULT 2

S74248

antibacterial peptide LL-37 precursor - human

N:Alternate names: antibacterial peptide FALL39

N:Contains: antibacterial peptide LL-37; cathelin-related antibacterial peptide CAP-18

C:Species: Homo sapiens (man)

C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004

C:Accession: S74248; S78211; S66281; S66205; A55596; S49441; S58023

R:Gudmundsson, G.H.; Agerberth, B.; Odeberg, J.; Bergman, T.; Olsson, B.; Salcedo, R.

Eur. J. Biochem. 238, 325-332, 1996

A:Title: The human gene FALL39 and processing of the cathelin precursor to the antibacte

A:Reference number: S74248; MUID:96283824; PMID:8681941

A:Accession: S74248

A:Molecule type: DNA

A:Residues: 1-170 <GUD>

A:Cross-references: UNIPROT:P49913; UNIPARC:UPI0000017636C; EMBL:X96735

A:Accession: S78211

A;Molecule type: protein
A;Residues: 134-143 <GUE>
A;Cross-references: UNIPARC:UPI0000017636D
R;Cowland, J.B.; Johnsen, A.H.; Borregaard, N.
FEBS Lett. 368, 173-176, 1995
A;Title: hCAP-18, a cathelin/pro-bactenecin-like protein of human neutrophil specific granules
A;Reference number: S66205; MUID:95339969; PMID:7615076
A;Accession: S66281
A;Molecule type: mRNA
A;Residues: 1-112, 'T', 114-170 <COW>
A;Cross-references: UNIPARC:UPI00000000A67; EMBL:X89658; NID:G902627; PIDN:CAA61805.1; PI
A;Accession: S66205
A;Molecule type: protein
A;Residues: 42-49; 50-57; 58-65, 'X', 67-85, 'X', 87-96, 'X', 98-100; 110-112, 'T', 114-152 <COF>
A;Cross-references: UNIPARC:UPI000017636E; UNIPARC:UPI000017636F; UNIPARC:UPI0000176370;
R;Agierberth, B.; Gunne, H.; Odeberg, J.; Kogner, P.; Boman, H.G.; Gudmundsson, G.H.
Proc. Natl. Acad. Sci. U.S.A. 92, 195-199, 1995
A;Title: FAUL-19, a putative human peptide antibiotic, is cysteine-free and expressed in
A;Reference number: A55596; MUID:95116523; PMID:7529412
A;Accession: A55596
A;Molecule type: mRNA
A;Residues: 1-5, 'N', 7-112, 'T', 114-170 <AGE>
A;Cross-references: UNIPARC:UPI000000D841; EMBL:Z38026; NID:G558378; PIDN:CAA86115.1; PI
C;Genetics:
A;Gene: FALL39
A;Map position: 3
A;Introns: 67/3, 103/3, 127/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: antibacterial; blocked amino end; pyroglutamic acid
F;1-30/Domain: signal sequence #status predicted <SIW>
F;22-130/Domain: cystatin homology <CYS>
F;31-170/Domain: cathelin-related antibacterial peptide CAP-18 #status predicted <MAT1>
F;31-133/Domain: propeptide #status predicted <PRO>
F;314-170/Product: antibacterial peptide Lb-37 #status experimental <MAT>
F;31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 99.4%; Score 874; DB 2; Length 170;
Best Local Similarity 99.4%; Pred. No. 2.7e-76;
Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
Db 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60

Qy 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Db 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120

Qy 121 FDISCDKDKRFPALLGDFPRKSKKIGKFKRIVORIKDFLRNLVPTRES 170
Db 121 FDISCDKDKRFPALLGDFPRKSKKIGKFKRIVORIKDFLRNLVPTRES 170

RESULT 3
JQ1171
18K lipopolysaccharide-binding protein precursor - rabbit
N;Alternate names: 18K cationic protein
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
C;Accession: JQ1171; PS0226
R;Larrick, J.W.; Morgan, J.G.; Fallings, I.; Hirata, M.; Yen, M.H.
Biochem. Biophys. Res. Commun. 179, 170-175, 1991
A;Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding
A;Reference number: JQ1171; MUID:91354246; PMID:1883348
A;Accession: JQ1171
A;Molecule type: mRNA
A;Residues: 1-171 <LAR>
A;Cross-references: UNIPARC:UPI00000145211
A;Experimental source: bone marrow
A;Accession: PS0226
A;Molecule type: protein
A;Residues: 135-159, 'QIGQLL' <LA2>
A;Cross-references: UNIPARC:UPI0000176372

A;Note: 157-Asp was also found
C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 53.0%; Score 465.5; DB 2; Length 171;
Best Local Similarity 57.3%; Pred. No. 3.5e-37;
Matches 98; Conservative 26; Mismatches 44; Indels 3; Gaps 2;

Qy 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
Db 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 59

Qy 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Db 60 MDPOLEDAKDYTPQVSTVKETECRTTWKLFQCDKFEDGLVKRCMGVTTRYQAWDS 119

Qy 121 FDISCDK--DNKRFPALLGDFPRKSKKIGKFKRIVORIKDFLRNLVPTRE 169
Db 120 FDIRCNAQESPEPTGLRKLRFKRNKIKKIKGKIQGLPKLAPRTD 170

RESULT 4
S68967
antibacterial peptide - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S68967
R;Tossi, A.; Scocchi, M.; Zanetti, M.; Storici, P.; Gennaro, R.
Eur. J. Biochem. 228, 941-946, 1995
A;Title: PMAP-37, a novel antibacterial peptide from pig myeloid cells. cDNA cloning, ch
A;Reference number: S68967; MUID:95255306; PMID:7737198
A;Accession: S68967
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-167 <TOS>
A;Cross-references: UNIPROT:P49932; UNIPARC:UPI000012F429; EMBL:L39641; NID:G703244; PID
C;Superfamily: cathelin; cystatin homology
F;22-129/Domain: cystatin homology <CYS>

Query Match 50.6%; Score 444.5; DB 2; Length 167;
Best Local Similarity 57.1%; Pred. No. 3.5e-35;
Matches 92; Conservative 26; Mismatches 40; Indels 3; Gaps 2;

Qy 1 MKTQDGHSLGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
Db 1 METQRASLCIGRWSLVLLGLVMPPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLE 59

Qy 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Db 60 LDQPPKADEDFGTPKPVSTVKETVCPRTWRPELDFKENGVRVKQCVGTTLQDKIP 119

Qy 121 FDISCDKDKN--RFPALLGDFPRKSKKIGKFKRIVORIKD 159
Db 120 LDITCNEIQSVGLSLRLRDLFLSDGRRLGKIERIGQIKD 160

RESULT 5
S41731
antibacterial protein precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S41731
R;Storici, P.; Scocchi, M.; Tossi, A.; Gennaro, R.; Zanetti, M.
FEBS Lett. 337, 303-307, 1994
A;Title: Chemical synthesis and biological activity of a novel antibacterial peptide ded
A;Reference number: S41731; MUID:94123775; PMID:8293820
A;Accession: S41731
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-166 <STO>
A;Cross-references: UNIPROT:P49931; UNIPARC:UPI000012F428; GB:L29125; NID:G457347; PIDN:
C;Superfamily: cathelin; cystatin homology

F;22-129/Domain: cystatin homology <CYS>

Query Match 50.5%; Score 443.5; DB 2; Length 166;
Best Local Similarity 61.3%; Pred. No. 4.3e-35;
Matches 95; Conservative 18; Mismatches 39; Indels 3; Gaps 2;
Qy 1 MKTQDGHSLGRWSLVLLGLVMPALIAIQAQLSVYKRAVLRAIDGINQRSSDANLYRLLD 60
Db 1 METQASISLGRWSLVLLGLVMPALIAIQAQLSVYKRAVLRAIDGINQRSSDANLYRLLE 59
Qy 61 LDPRTMDGDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTVTLNQARGS 120
Db 60 LDQPKAEDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTVTLNQARGS 119
Qy 121 FDISCDK 153
Db 120 LDINCDEIQSVGRFRRLAKTKRLKIKGKVLKI 154

RESULT 6

A53421
antibacterial peptide precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: A53421
R;Zanetti, M.; Storici, P.; Tossi, A.; Scocchi, M.; Gennaro, R.
J. Biol. Chem. 269, 7855-7858, 1994
A;Title: Molecular cloning and chemical synthesis of a novel antibacterial peptide derived from the sheep myeloid cathelicidin
A;Reference number: A53421; MUID:94179144; PMID:8132502
A;Accession: A53421
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-153 <ZAN>
A;Cross-references: UNIPROT:P49930; UNIPARC:UPI000012F425; GB:L26053; NID:9468911; PIDN:
C;Superfamily: cathelin; cystatin homology
C;Keywords: antibacterial
F;22-129/Domain: cystatin homology <CYS>

Query Match 49.9%; Score 438.5; DB 2; Length 153;
Best Local Similarity 67.7%; Pred. No. 1.2e-34;
Matches 86; Conservative 19; Mismatches 21; Indels 1; Gaps 1;
Qy 1 MKTQDGHSLGRWSLVLLGLVMPALIAIQAQLSVYKRAVLRAIDGINQRSSDANLYRLLD 60
Db 1 METQASISLGRWSLVLLGLVMPALIAIQAQLSVYKRAVLRAIDGINQRSSDANLYRLLE 59
Qy 61 LDPRTMDGDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTVTLNQARGS 120
Db 60 LDQPKAEDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTVTLNQARGS 119
Qy 121 FDISCDK 127
Db 120 FDIITCN 126

RESULT 7

S68229
antimicrobial peptide precursor - sheep
N;Alternate names: procyclic dodecapeptide homolog
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68229
R;Bagella, L.; Scocchi, M.; Zanetti, M.
FEBS Lett. 376, 225-228, 1995
A;Title: cDNA sequences of three sheep myeloid cathelicidins.
A;Reference number: S68228; MUID:96105386; PMID:7498547
A;Accession: S68229
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <BAG>
A;Cross-references: UNIPROT:P54230; UNIPARC:UPI0000126859; EMBL:L46853; NID:g1161246; PI
C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>

F;22-129/Domain: cystatin homology <CYS>
F;29-143/Domain: propeptide #status predicted <PRO>
F;144-155/Product: antimicrobial peptide #status predicted <MAT>

Query Match 49.2%; Score 432.5; DB 2; Length 155;
Best Local Similarity 68.3%; Pred. No. 4.5e-34;
Matches 86; Conservative 18; Mismatches 21; Indels 1; Gaps 1;
Qy 1 MKTQDGHSLGRWSLVLLGLVMPALIAIQAQLSVYKRAVLRAIDGINQRSSDANLYRLLD 60
Db 1 METQASISLGRWSLVLLGLVMPALIAIQAQLSVYKRAVLRAIDGINQRSSDANLYRLLE 59
Qy 61 LDPRTMDGDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTVTLNQARGS 120
Db 60 LDQPKAEDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTVTLNQARGS 119
Qy 121 FDISCD 126
Db 120 FDIITCN 125

RESULT 8

S70521
cathelin-related protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70521
R;Popova, A.B.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlman, J.M.J.M.; Fibbe, W.E.; Bely
FEBS Lett. 391, 5-8, 1996
A;Title: A novel murine cathelin-like protein expressed in bone marrow.
A;Reference number: S70521; MUID:96326596; PMID:8706928
A;Accession: S70521
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-173 <POP>
A;Cross-references: UNIPROT:P51437; UNIPARC:UPI0000049482; EMBL:X94353; NID:g1177533; PI
C;Superfamily: cathelin; cystatin homology
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-144/Domain: propeptide #status predicted <PRO>
F;145-173/Product: cathelin-related protein #status predicted <MAT>

Query Match 49.1%; Score 431.5; DB 2; Length 173;
Best Local Similarity 52.6%; Pred. No. 6.4e-34;
Matches 92; Conservative 23; Mismatches 51; Indels 9; Gaps 2;
Qy 1 MKTQDGHSLGRWSLVLLGLVMPALIAIQAQLSVYKRAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MQFQDVPSELWLSLSLLLLGNG---FSQTPSYRDAVLRAVDVFNQSLDTNLYRLLD 57
Qy 61 LDPRTMDGDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTVTLNQARGS 120
Db 58 LDQPKAEDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTVTLNQARGS 117
Qy 121 FDISCDKN-----KRPALLGDPFRKSKKIGKFKRIQRIKDFLRNLVPRTE 169
Db 118 FDISCNFQAQPFPRFKKISRLAGLLRKGGKIGKFKRIQRIKDFLRNLVPRTE 172

RESULT 9

S40463
prophenin (PF-2) precursor - pig
N;Alternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40463; S57331; S68233
R;Pungercar, J.; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk,
FEBS Lett. 336, 284-288, 1993
A;Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial
A;Reference number: S40463; MUID:94085623; PMID:8262247
A;Accession: S40463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-228 <PUN>

F;144-155/Product: bactenecin #status experimental <MAT>
F;146-154/Disulfide bonds: #status experimental

Query Match	48.6%	Score	427.5;	DB 2;	Length	155;	
Best Local Similarity	66.7%	Pred. No.	1.4e-33;				
Matches	84;	Conservative	18;	Mismatches	23;	Gaps	1;

QY 1 MKTQRGHSIGRWSLVLLILGLVMPALIAIQVLVSKEAVLRALDGINQRSSDANLYRLLD 60
Db 1 METPRASLSIGRWSLWLLIIGLALPSA-SAAQLSVEARVLRDAVDQLNQESSEPNRYRLE 59
|||
QY 61 LDRPRTMDGDPTPKSVSFVKETVCPRFTQQSPEDCDKDCGLVKRCMGTVTLNQARGS 120
Db 60 LDQPFPQDEDPDKRSVRVKETVCSTRTTQPPQCDFKENGLLKRCBGTVTLDQVRGN 119
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QY 121 FDISC 126
Db 120 FDITCN 125
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|||:

RESULT 11

S68232

N;Antimicrobial protein PR-39 precursor, cathelin-associated - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68232; JN0899; I47138; S19563
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
PEBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides
A;Reference number: S68232; MUID:96105365; PMID:7498526
A;Accession: S68232
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-172 <ZHA>
A;Cross-references: UNIPROT:P80054; UNIPARC:UPI000013215B; EMBL:X89201; NID:g11
A;Experimental source: leukocytes
R;Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical
A;Reference number: JN0899; MUID:94071853; PMID:8250863
A;Accession: JN0899
A;Molecule type: mRNA
A;Residues: 1-20,'A','22-172 <STO>
A;Cross-references: UNIPARC:UPI000016C6E7; GB:L23825; NID:G435100; PIDN:AAA3110
R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin
A;Reference number: I47138; MUID:95350216; PMID:7624374
A;Accession: I47138
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: DNA
A;Residues: 1-28,'T','30-89,'QR','92-116,'NDP','120-172 <GUD>
A;Cross-references: UNIPARC:UPI000016C6AC; EMBL:X87236; NID:G829142; PIDN:CAA60
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.;
Eur. J. Biochem. 202, 849-854, 1991
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new mem
A;Reference number: S19563; MUID:92111534; PMID:1765098
A;Accession: S19563
A;Molecule type: protein
A;Residues: 131-169 <AGE>
A;Cross-references: UNIPARC:UPI000002D613
A;Experimental source: intestine
C;Genetics:
A;Gene: PR39
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

A:Reference number: JN0900; MUID:94071998; PMID:8250892

A:Accession: JN0900

A:Molecule type: mRNA

A:Residues: 1-147 <STO>

A:Cross-references: UNIPROT:P32195; UNIPARC:UPI0000131776; GB:L24745; NID:9431435; PIDN: R:Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, FEBS Lett. 330, 339-342, 1993

A:Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence

A:Reference number: S36820; MUID:93387466; PMID:8375505

A:Accession: S36822

A:Molecule type: protein

A:Residues: 131-146 <MIR>

A:Cross-references: UNIPARC:UPI000014310F

R:Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alezhina, G.M.; Sh

FEBS Lett. 327, 231-236, 1993

A:Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost

A:Reference number: S34585; MUID:93327946; PMID:8335113

A:Accession: S34586

A:Molecule type: protein

A:Residues: 131-146 <KOK>

A:Cross-references: UNIPARC:UPI000014310F

C:Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism

C:Superfamily: cathelin; cystatin homology

C:Keywords: amidated carboxyl end; antibacterial; neutrophil

F:1-29/Domain: signal sequence #status predicted <SIG>

F:22-129/Domain: cystatin homology <CYS>

F:131-146/Product: protegrin 2 #status experimental <MAT>

F:146/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl

Query Match 47.6%; Score 418.5; DB 2; Length 147;

Best Local Similarity 65.4%; Pred. No. 9.3e-33;

Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

Qy 1 MKTORDGHSGLRWSLVLLLLGLVMPALIAIQVLVSKEAVLRALDGINQRSSDANLYRLLD 60

Db 1 METQBASICLGWSLWLLLLLWVPSA-SQAQLSYREAVLRVDRNLNESSEANLYRLLE 59

Qy 61 LDRPTMDGDPDPKPVSVFTVKETVCPRPTQGSPEBCDFPKKGGLVKKCMGFTVTLNQARGS 120

Db 60 LDQPPKADDPGTPKPVSVFTVKETVCPRPTQPPPELCLDFKENGVRVKQCVGVTTLQIKDP 119

Qy 121 FDISCDK 127

Db 120 LDITCNE 126

RESULT 14

A53895

protegrin 3 precursor - pig

N:Alternate names: neutrophil peptide 2

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 01-Dec-1995 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004

C:Accession: S66285; A53895; S34587; S36821; S57608

R:Zhao, C.; Ganz, T.; Lehrer, R.I.

FEBS Lett. 368, 197-202, 1995

A:Title: The structure of porcine protegrin genes.

A:Reference number: S66283; MUID:95354835; PMID:7628604

A:Accession: S66285

A:Molecule type: DNA

A:Residues: 1-149 <ZH3>

A:Cross-references: UNIPROT:P32196; UNIPARC:UPI0000131777; EMBL:X84095; NID:9887644; PID

R:Zhao, C.; Liu, L.; Lehrer, R.I.

FEBS Lett. 346, 285-288, 1994

A:Title: Identification of a new member of the protegrin family by cDNA cloning.

A:Reference number: S45712; MUID:94283613; PMID:8013647

A:Accession: A53895

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-149 <ZHA>

A:Cross-references: UNIPARC:UPI0000131777; GB:X83267; NID:9603037; PIDN:CAA58240.1; PID:

R:Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Alezhina, G.M.; Sh

FEBS Lett. 327, 231-236, 1993

A:Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost

A;Reference number: S34585; MUID:93327946; PMID:8335113
A;Accession: S34587
A;Molecule type: protein
A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UPI0000143110
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, F.B.S Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: S36820; MUID:93387466; PMID:8375505
A;Accession: S36821
A;Molecule type: protein
A;Residues: 131-148 <MIR>
A;Cross-references: UNIPARC:UPI0000143110
C;Genetics:
A;Gene: NPG3
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 47.6%; Score 418.5; DB 2; Length 149;
Best Local Similarity 65.4%; Pred. No. 9.5e-33;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
Db 1 METQRASLCGLRWSLWLLLLALVVPESA-SQAQALSYREAVLRAVDRLNEQSSEANLYRLLE 59
Qy 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 120
Db 60 LDQPPKADEDPGTTPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 119
Qy 121 FDISCDK 127
Db 120 LDIITCNE 126

RESULT 15
S57607
protegrin 1 precursor - pig
N;Alternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56284; S45712; S36820; S34585; S57607
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S56283; MUID:95354835; PMID:7628604
A;Accession: S56284
A;Molecule type: DNA
A;Residues: 1-149 <ZHA>
A;Cross-references: UNIPROT:P32194; UNIPARC:UPI0000131775; EMBL:X84094; NID:9887642; PID
R;Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613; PMID:8013647
A;Accession: S45712
A;Molecule type: mRNA
A;Residues: 1-149 <ZH2>
A;Cross-references: UNIPARC:UPI0000131775; GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, F.B.S Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: S36820; MUID:93387466; PMID:8375505
A;Accession: S36820
A;Molecule type: protein
A;Residues: 131-148 <MIR>
A;Cross-references: UNIPARC:UPI0000034C2E
R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; SH

FEBS Lett. 327, 231-236, 1993
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A;Reference number: S34585; MUID:93327946; PMID:8335113
A;Accession: S34585
A;Molecule type: protein
A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UPI0000034C2E
C;Genetics:
A;Gene: NPG1
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 1 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 47.6%; Score 418.5; DB 2; Length 149;
Best Local Similarity 65.4%; Pred. No. 9.5e-33;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPALIAIQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
Db 1 METQRASLCGLRWSLWLLLLALVVPESA-SQAQALSYREAVLRAVDRLNEQSSEANLYRLLE 59
Qy 61 LDPRTMDGDDPTPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 120
Db 60 LDQPPKADEDPGTTPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 119
Qy 121 FDISCDK 127
Db 120 LDIITCNE 126

Search completed: January 12, 2006, 21:51:07
Job time : 16.0554 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2006, 21:42:24 ; Search time 82.8044 Seconds
(without alignments)
1448.471 Million cell updates/sec

Title: US-10-815-562-2

Perfect score: 879

Sequence: 1 MKTQDGHSGHWSLVLLLL.....KRIVQRIKDFLRLVPRTES 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	879	100.0	170	1	FAL39_HUMAN
2	879	100.0	170	1	FAL39_MACMU
3	759	86.3	170	2	Q9GLV5_MACMU
4	498.5	56.7	157	2	O62841_HORSE
5	486.5	55.3	172	2	O6TN20_CANEA
6	468.5	53.3	171	1	CAP18_FABIT
7	457.5	52.0	170	2	O62842_HORSE
8	454	51.6	165	1	BNA34_BOVIN
9	453.5	51.6	171	2	Q71KM5_RAT
10	451	51.3	156	2	O62840_HORSE
11	444.5	50.6	167	1	PMP37_PIG
12	443.5	50.5	166	1	PMP36_PIG
13	442.5	50.3	176	1	BCTN5_CAPHI
14	442.5	50.3	176	2	Q4JFB9_CAPHI
15	440	50.1	165	2	P79360_SHEEP
16	438.5	49.9	153	1	PMP23_PIG
17	437.5	49.8	176	1	BCTN5_SHEEP
18	433.5	49.3	173	1	CRAMP_MOUSE
19	432.5	49.2	155	1	BCTN1_SHEEP
20	432	49.1	158	1	BNA27_BOVIN
21	432	49.1	159	1	BNA28_BOVIN
22	431	49.0	165	2	P82017_CAPHI
23	429.5	48.9	228	1	PF12_PIG
24	427.5	48.6	155	1	BCTN1_BOVIN
25	427.5	48.6	172	1	PR39_PIG
26	424.5	48.3	149	1	PG5_PIG
27	418.5	47.6	147	1	PG2_PIG
28	418.5	47.6	149	1	PG1_PIG
29	418.5	47.6	149	1	PG3_PIG
30	418.5	47.6	149	1	PG4_PIG
31	416.5	47.4	190	1	BCTN7_BOVIN

32	413	47.0	158	2	Q9XSQ8_CAPHI
33	412	46.9	160	1	SC51_SHEEP
34	410.5	46.7	176	1	BCTN5_BOVIN
35	406.5	46.2	144	2	Q683R8_BUBBU
36	405.5	46.1	144	1	INDC_BOVIN
37	400	45.5	160	1	SC52_SHEEP
38	387.5	44.1	212	1	PF11_PIG
39	385.5	43.9	190	2	Q9XSQ9_CAPHI
40	380.5	43.3	164	2	P79361_SHEEP
41	374.5	42.6	190	1	BCTN7_SHEEP
42	369.5	42.0	224	2	O19031_SHEEP
43	360.5	41.0	182	2	O19040_SHEEP
44	325	37.0	178	2	Q91X12_CAVPO
45	322.5	36.7	109	2	Q920X4_MUSSI

ALIGNMENTS

RESULT 1
FAL39_HUMAN
ID FAL39_HUMAN STANDARD; PRT; 170 AA.
AC P49913;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein FAL39 precursor (FAL39 peptide antibiotic)
DE (Cationic antimicrobial protein CAP-18) (hCAP-18) [Contains:
DE Antibacterial protein LL-37].
GN Name=CAMP; Synonyms=CAP18, FALL39;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
RX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND SYNTHESIS OF 132-170.
RC TISSUE=Bone marrow;
RX MEDLINE=95116523; PubMed=7529412;
RA Agerberth B., Gunne H., Odeberg J., Kogner P., Roman H.G.,
RA Gudmundsson G.H.;
RT "FALL-39, a putative human peptide antibiotic, is cysteine-free and
RT expressed in bone marrow and testis.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:195-199(1995).
[2]
RC TISSUE=Bone marrow;
RX MEDLINE=95339969; PubMed=7615076; DOI=10.1016/0014-5793(95)00634-L;
RA Cowland J.B., Johnsen A.H., Borregaard N.;
RT "hCAP-18, a cathelin/pro-bactenecin-like protein of human neutrophil
RL specific granules.";
RL FEBS Lett. 368:173-176(1995).
[3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Bone marrow;
RX MEDLINE=95197251; PubMed=7890387;
RA Larrick J.W., Hirata M., Balint R.F., Lee J., Zhong J., Wright S.C.;
RT "Human CAP18: a novel antimicrobial lipopolysaccharide-binding
RT protein.";
RL Infect. Immun. 63:1291-1297(1995).
[4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=97102716; PubMed=8946956; DOI=10.1016/S0014-5793(96)01199-4;
RA Larrick J.W., Lee J., Ma S., Li X., Francke U., Wright S.C.,
RA Balint R.F.;
RT "Structural, functional analysis and localization of the human CAP18
RT gene.";
RL FEBS Lett. 398:74-80(1996).
[5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=8681941;
RA Gudmundsson G.H., Agerberth B., Odeberg J., Bergman T., Olsson B.,
RA Salcedo R.;

"The human gene FALL39 and processing of the cathelin precursor to the antibacterial peptide LL-37 in granulocytes.",
Eur. J. Biochem. 238:325-332(1996).
[6]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Epithelium;
RA Gao Y., Huang Y.F., Xia X.Y.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
[7]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Testis;
RA Wu N., Miao S.Y., Zhang X.D., Qiao Y., Liang G., Wang L.F.;
RL "A new spermatogenesis-related gene."
[8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Kohn B., Zuo D., Hu Y., LaBaer J.;
RL "Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)."
[9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marais K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzyski M.I., Skalska U., Smal M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
[10]
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in bone marrow and testis and neutrophils.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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DR EMBL; Z38026; CRA86115.1; -; mRNA.
DR EMBL; X89658; CRA61805.1; -; mRNA.
DR EMBL; U19970; AAA74084.1; -; mRNA.
DR EMBL; U48795; AAC02634.1; -; Genomic DNA.
DR EMBL; X96735; -; NOT_ANNOTATED_CDS; Genomic DNA.
DR EMBL; AY162210; AAN78318.1; -; mRNA.
DR EMBL; AY251531; AAP20054.1; -; mRNA.
DR EMBL; CR457083; CAG33364.1; -; mRNA.
DR EMBL; CR541961; CAG46759.1; -; mRNA.
DR EMBL; BC055089; AAH55089.1; -; mRNA.
DR PIR; I38932; I38932.
DR PIR; S74248; S74248.
DR HSGP; P32196; 1KWI.
DR Ensembl; ENSG00000164047; Homo sapiens.

DR HGNC; HGNC:1472; CAMP.
DR MIM; 600474; -.
DR GO; GO:0042742; P:defense response to bacteria; TAS.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidin; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antibiotic; Antimicrobial; Direct protein sequencing;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 30 Potential.
FT PROPEP 31 131
FT CHAIN 132 170 Antibacterial protein FALL-39.
FT CHAIN 134 170 Antibacterial protein LL-37.
FT MOD_RES 31 31 Pyrrolidone carboxylic acid (By similarity).
FT DISULFID 86 97 By similarity.
FT DISULFID 108 125 By similarity.
FT CONFLICT 6 6 D -> N (in Ref. 1, 6, 7 and 8; CAG46759).
SQ SEQUENCE 170 AA; 19301 MW; 055B07DCA95A7D16 CRC64;

Query Match 100.0%; Score 879; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.9e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTQDGHSLGRWSLVLLLLGLVNPFLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
DB 1 MKTQDGHSLGRWSLVLLLLGLVNPFLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60

QY 61 LDPRTTMDGDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
DB 61 LDPRTTMDGDDPTPKPVSTVKTVCPTTQSPEDCDPKDGLVKRCMGVTTLNQARGS 120

QY 121 FDISCDKDKRFPALLGDFFRKSKKIGKPKRIQVRIKDFLRNLVPRTES 170
DB 121 FDISCDKDKRFPALLGDFFRKSKKIGKPKRIQVRIKDFLRNLVPRTES 170

RESULT 2
FALL39_MACMU STANDARD; PRT; 170 AA.
AC Q71SN9;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial protein FALL-39 precursor (FALL-39 peptide antibiotic)
DE Cationic antimicrobial protein CAP-18 (rhcAP-18) [Contains:
DE Antibacterial protein LL-37 (rhlL-37)].
GN Name=CAMP; Synonyms=CAP18, FALL39;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chordata; Eumarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.
RX MEDLINE=21137962; PubMed=11238224; DOI=10.1128/CDLI.8.2.370-375.2001;
RA Bais R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
RL "Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are close homologues of human molecules."
RL Clin. Diagn. Immunol. 8:370-375(2001).
CC -!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has antibacterial activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in epithelia of various organs. Most abundant peptide levels are found in organs lining outer or inner body surfaces, such as organs of the respiratory or gastrointestinal tract.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL; AF288284; AAG40802.1; -, mRNA.
 DR InterPro; IPR001894; Cathelicidin.
 DR PANTHER; PTHR10206; Cathelicidin; 1.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidins; 1.
 DR PROSITE; PS00946; CATHELICIDINS_2; 1.
 DR PROSITE; PS00947; CATHELICIDINS_1; 1.
 KW Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
 FT SIGNAL 1 30 Potential.
 FT PROPEP 31 131 Potential.
 FT CHAIN 132 170 Antibacterial protein FALL-39.
 FT CHAIN 134 170 Antibacterial protein LL-37.
 FT MOD_RES 31 31 Pyrrolidone carboxylic acid (By
 FT similarity).
 SQ SEQUENCE 170 AA; 19301 MW; 055B07DCA95A7D16 CRC64;

Query Match 100.0%; Score 879; DB 1; Length 170;
 Best Local Similarity 100.0%; Pred. No. 6.9e-76;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRADGINQRSSDANLYRLLD 60
 Db 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRADGINQRSSDANLYRLLD 60
 Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGKGLVKRCMGTVTLLNQARGS 120
 Db 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGKGLVKRCMGTVTLLNQARGS 120
 Qy 121 FDISCDKDKRKFALLGDFPRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170
 Db 121 FDISCDKDKRKFALLGDFPRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170

RESULT 3

O9GLV5 MACMU
 ID O9GLV5 MACMU PRELIMINARY; PRT; 170 AA.
 AC O9GLV5
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Cathelin.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopitheidae; Cercopithecinæ; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow;
 RX MEDLINE=21441139; PubMed=11557457;
 RX DOI=10.1128/JAC.45.10.2695-2702.2001;
 RA Zhao C., Nguyen T., Boo L.M., Hong T., Espiritu C., Orlov D., Wang W.,
 RA Waring A., Lehrer R.I.;
 RT "RL-37, an alpha-helical antimicrobial peptide of the rhesus monkey."
 RL Antimicrob. Agents Chemother. 45:2695-2702(2001).
 DR EMBL; AF181954; AAG09440.1; -, mRNA.
 DR HSSP; P32196; 1KWI.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 SQ SEQUENCE 170 AA; 18861 MW; 355AB3BF510DBB83 CRC64;

Query Match 86.3%; Score 759; DB 2; Length 170;
 Best Local Similarity 86.5%; Pred. No. 2.1e-64;

Matches 147; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRADGINQRSSDANLYRLLD 60
 Db 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRADGINQRSSDANLYRLLD 60
 Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGKGLVKRCMGTVTLLNQARGS 120
 Db 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGKGLVKRCMGTVTLLNQARGS 120
 Qy 121 FDISCDKDKRKFALLGDFPRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170
 Db 121 FDISCDKDKRKFALLGDFPRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170

RESULT 4

O62841 HORSE
 ID O62841 HORSE PRELIMINARY; PRT; 157 AA.
 AC O62841
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Myeloid cathelicidin 2 precursor.
 GN Name=eCATH-2;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Bone marrow;
 RX MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
 RA Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
 RA Zanetti M.;
 RT "Novel cathelicidins in horse leukocytes."
 RL FEBS Lett. 457:459-464(1999).
 DR EMBL; AJ224928; CAAL2227.1; -, mRNA.
 DR HSSP; P32196; 1KWI.
 DR SMR; O62841; 30-130.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS_1; 1.
 DR PROSITE; PS00947; CATHELICIDINS_2; 1.
 KW Signal.
 FT SIGNAL 1 29 Potential.
 FT CHAIN 30 157 myeloid cathelicidin 2.
 SQ SEQUENCE 157 AA; 18153 MW; 1424C493D2B307CC CRC64;

Query Match 56.7%; Score 498.5; DB 2; Length 157;

Best Local Similarity 76.4%; Pred. No. 1.7e-39;
 Matches 97; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQVLSYKEAVLRADGINQRSSDANLYRLLD 60
 Db 1 METQDSCSLGRWSLVLLLLGLVNPPLA-TTQVLSYKEAVLRADGINQRSSDANLYRLLE 59
 Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGKGLVKRCMGTVTLLNQARGS 120
 Db 60 LDPLPKEDDDPTPKPVSFTVKETVCPRTTQOQPLEECDFKENGVLKQCVGTVLDPAKDY 119
 Qy 121 FDISCDK 127
 Db 120 FDISCDK 126

RESULT 5

O6TN20 CANFA
 ID O6TN20 CANFA PRELIMINARY; PRT; 172 AA.
 AC O6TN20;

DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Cathelicidin.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sang Y., Rune K., Melgarejo T., Blecha F.;
 RL Submitted (S8P-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY392089; AAR26245.1; -; mRNA.
 DR Ensembl; ENSCAPG0000012896; Canis familiaris.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IPR001894; Cathelicidin.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 SQ SEQUENCE 172 AA; 19437 MW; 549EAC408DB7A63 CRC64;

 Query Match 55.3%; Score 486.5; DB 2; Length 172;
 Best Local Similarity 57.9%; Pred. No. 2.7e-38;
 Matches 99; Conservative 27; Mismatches 42; Indels 3; Gaps 2;

 Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPPLAIIAQVLSYKEAVLRADGINQRSDANLYRLLD 60
 Db 1 METQKPSLGRWSLVLLLLGLVITPA-ASRALSRYEAVLRVNGFNQRSEENLYRLIQ 59

 Qy 61 LDPRTWDGDDPTPKPVSVFTVKETVCPRTTQSQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
 Db 60 LNSQPKGEDNIPFAPVSVFTVKETVCPRTTQSQSPEDCDPKDGLVKRCMGVTTLNQARGS 119

 Qy 121 FDISCDK--DNKRFPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLYPRTE 169
 Db 120 FDLNCDSLQVKKIDRLKELITGQKIGEKIRRIQRIKDFRNLYQPRE 170

 RESULT 6
 ID CAP18 RABIT STANDARD; PRT; 171 AA.
 AC P25230;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-
 binding protein) (18 kDa cationic protein) (CAP18-A) [Contains:
 Antimicrobial protein CAP7].
 DE Name=CAP18;
 GN Oryctolagus cuniculus (Rabbit).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 135-159.
 RC TISSUE=Bone marrow;
 RA Larick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
 RX MEDLINE=91354246; PubMed=1883348;
 RT "Complementary DNA sequence of rabbit CAP18 -- a unique
 lipopolysaccharide binding protein.";
 RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
 [2]
 RP PROTEIN SEQUENCE OF 135-159, AND CHARACTERIZATION.
 RX MEDLINE=94178952; PubMed=8132348;
 RA Hirata M., Shimamura Y., Yoshida M., Morgan J.G., Palings I.,
 RA Wilson D., Yen M.H., Wright S.C., Larick J.W.;
 RT "Characterization of a rabbit cationic protein (CAP18) with
 lipopolysaccharide-inhibitory activity.";
 RL Infect. Immun. 62:1421-1426(1994).
 RN [3]

RP PROTEIN SEQUENCE OF 135-154, AND CHARACTERIZATION.
 RX MEDLINE=94075827; PubMed=8254193;
 RA Larick J.W., Hirata M., Zheng H., Zhong J., Bolin D.,
 RA Cavallion J.-M., Warren H.S., Wright S.C.;
 RT "A novel granulocyte-derived peptide with lipopolysaccharide-
 neutralizing activity.";
 RL J. Immunol. 152:231-240(1994).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
 RA Tossi A., Scocchi M., Skerlavaj B., Gennaro R.;
 RT "Identification and characterization of a primary antibacterial domain
 in CAP18, a lipopolysaccharide binding protein from rabbit
 leukocytes.";
 RL FEBS Lett. 339:108-112(1994).
 RN [5]
 RP STRUCTURE BY NMR OF 135-166.
 RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
 RA Chen C., Brock R., Luh F., Chou P.-J., Larick J.W., Huang R.-P.,
 RA Huang T.-H.;
 RT "The solution structure of the active domain of CAP18 -- a
 lipopolysaccharide binding protein from rabbit leukocytes.";
 RL FEBS Lett. 370:46-52(1995).
 CC CAP18 binds to the lipid moiety of bacterial
 lipopolysaccharides (LPS), a glycolipid present in the outer
 membrane of all Gram-negative bacteria. Has antibiotic activity.
 CC -!- FUNCTION: CAP18 binds to the lipid moiety of bacterial
 lipopolysaccharides (LPS), a glycolipid present in the outer
 membrane of all Gram-negative bacteria. Has antibiotic activity.
 CC -!- TISSUE SPECIFICITY: Neutrophils.
 CC -!- SIMILARITY: Belongs to the cathelicidin family.
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 removed.
 CC -----
 DR EMBL; AAA31187.1; -; mRNA.
 DR PDB; 1LYP; NMR; @=135-166.
 DR InterPro; IPR001894; Cathelicidin.
 DR PANTHER; PTHR10206; Cathelicidin; 1.
 DR Pfam; PF00666; Cathelicidins; 1.
 DR ProDom; PD001838; Cathelicidin; 1.
 DR PROSITE; PS00946; CATHELICIDINS 1; 1.
 DR PROSITE; PS00947; CATHELICIDINS 2; 1.
 KW 3D-structure; Antibiotic; Antimicrobial; Direct protein sequencing;
 KW Pyrolidone carboxylic acid; Signal.
 FT SIGNAL 1 29 Potential.
 FT CHAIN 30 171 Antimicrobial protein CAP18.
 FT CHAIN 135 171 Antimicrobial protein CAP7.
 FT MOD_RES 30 30 Pyrolidone carboxylic acid (By
 similarity).
 FT DISULFID 85 96 By similarity.
 FT DISULFID 107 124 By similarity.
 FT VARIANT 157 157 K -> D.
 SQ SEQUENCE 171 AA; 19805 MW; D7BF2103BCFB13C4 CRC64;

 Query Match 53.3%; Score 468.5; DB 1; Length 171;
 Best Local Similarity 57.3%; Pred. No. 1.4e-36;
 Matches 98; Conservative 27; Mismatches 43; Indels 3; Gaps 2;

 Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPPLAIIAQVLSYKEAVLRADGINQRSDANLYRLLD 60
 Db 1 METHKHGSPSLAWSLVLLLLGLLMPPLA-IAQDLTYREAVLRVADFQNSSEANLYRLLS 59

 Qy 61 LDPRTWDGDDPTPKPVSVFTVKETVCPRTTQSQSPEDCDPKDGLVKRCMGVTTLNQARGS 120
 Db 60 MDPQQLLEDAKPYTPQPVSVFTVKETVCPRTTQSQSPEDCDPKDGLVKRCMGVTTLNQARGS 119

 Qy 121 FDISCDK--DNKRFPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLYPRTE 169
 Db 120 FDIKCNRAQSPSPBTGLRKLRKLRFRNKIKELKKIKGKIQGVFKLAPRTD 170

 RESULT 7

```

062842 HORSE
ID O62842 HORSE PRELIMINARY; PRT; 170 AA.
AC O62842;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Myeloid cathelicidin 3 precursor.
GN Name=cATH-3;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
RA Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
RA Zanetti M.;
RT "Novel cathelicidins in horse leukocytes.";
RL FEBS Lett. 457:459-464(1999).
DR EMBL; AJ224929; CAA12228.1; -; mRNA.
DR HSSP; P32196; 1KWI.
DR SRR; O62842; 30-130.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 170 myeloid cathelicidin 3.
SQ SEQUENCE 170 AA; 19299 MW; 5C35F1FA2D112BC8 CRC64;

Query Match 52.0%; Score 457.5; DB 2; Length 170;
Best Local Similarity 57.2%; Pred. No. 1.6e-35;
Matches 95; Conservative 24; Mismatches 38; Indels 9; Gaps 3;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQLVSYKAVLRAIDGINORSSDANLYRLLD 60
Db 1 METQRTCLGRWSLVLLLLGLVNPPLAIIPPA-TTQALSYKAVLRAVDGLNQRSDENLYRLLE 59

Qy 61 LDRPRTMGDGDPTPKPVSVFTVKETVCPRTTQSPEDCDPKKDGKGLVKRCMGVTTLNQAGS 120
Db 60 LDPLPKGDGSDTPKPVSEVMYKTVCPRTTQSPEDCDPKKDGKGLVKRCMGVTTLNQAGS 119

Qy 121 FDISCDKDNK--KRFALLGDFFRKSEKIGKEFK-----RIVQRIK 158
Db 120 FDISCDKDNK--KRFALLGDFFRKSEKIGKEFK-----RIVQRIK 165

RESULT 8
BMA34_BOVIN
ID BMA34_BOVIN STANDARD; PRT; 165 AA.
AC P56425;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial peptide BMAP-34 precursor.
GN Name=BMAP34;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=98072398; PubMed=9409740; DOI=10.1016/S0014-5793(97)01310-0;
RX Scocchi M., Wang S., Zanetti M.;
RA "Structural organization of the bovine cathelicidin gene family and
RT identification of a novel member.";

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FEBS Lett. 417:311-315(1997).
-1- FUNCTION: Exerts a potent antimicrobial activity.
-1- TISSUE SPECIFICITY: Expressed in bone marrow myeloid cells, spleen
and testis.
-1- SIMILARITY: Belongs to the cathelicidin family.
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removed.
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EMBL; Y12729; CAA73261.1; -; Genomic_DNA.
EMBL; Y12728; CAA73261.1; JOINED; Genomic_DNA.
DR HSSP; P32196; 1KWI.
DR SRR; P56425; 30-129.
DR InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidins; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 130 Potential.
FT PEPTIDE 131 165 Antibacterial peptide BMAP-34.
FT MOD RES 30 30 Pyrrolidone carboxylic acid.
FT MOD RES 165 165 Glycine amide (Potential).
FT DISULFID 86 97 By similarity.
FT DISULFID 108 125 By similarity.
SQ SEQUENCE 165 AA; 18848 MW; 21F14A0A68C6FBF0 CRC64;

Query Match 51.6%; Score 454; DB 1; Length 165;
Best Local Similarity 60.0%; Pred. No. 3.3e-35;
Matches 99; Conservative 21; Mismatches 41; Indels 4; Gaps 3;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVNPPLAIIAQLVSYKAVLRAIDGINORSSDANLYRLLD 60
Db 1 METQRTCLGRWSLVLLLLGLVNPPLAIIPPA-TTQALSYKAVLRAVDGLNQRSDENLYRLLE 59

Qy 61 LDRPRTMGDGDPTPKPVSVFTVKETVCPRTTQSPEDCDPKKDGKGLVKRCMGVTTLNQAGS 119
Db 60 LDPPEDQDVHFGARKPVSVFTVKETVCPRTTQSPEDCDPKKDGKGLVKRCMGVTTRYWIRG 119

Qy 120 SFDISCDKDNK--FALLGDFFRKSEKIGKEFKRIVQRIKDFLR 162
Db 120 SFDISCDKDNK--FALLGDFFRKSEKIGKEFKRIVQRIKDFLR 164

RESULT 9
Q71KM5_RAT
ID Q71KM5_RAT PRELIMINARY; PRT; 171 AA.
AC Q71KM5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CRAMP (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Termon S., Tollin M., Olsson B., Svenberg T., Agerberth B.,
RA Gudmundsson G.H.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF484553; AA005977.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.

```

```
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
FT NON_TER 1
SQ SEQUENCE 171 AA; 19320 MW; 788F3DA9DF10E839 CRC64;

Query Match 51.6%; Score 453.5; DB 2; Length 171;
Best Local Similarity 55.6%; Pred. No. 3.8e-35;
Matches 95; Conservative 21; Mismatches 48; Indels 7; Gaps 2;

Qy 5 RDGSLGRWSLVLLLLGLVMPALAIQAQLSYKEAVLRADIGNORSSDANLYRLLDLPPR 64
Db 1 RDVPSLRWSLSLLLLGLGLPLT-VSQTLSTREAVLRVDDFNQOQLDNLRYRLLDLSE 59

Qy 65 PTMGDDPTPKPVSTFKVETCPRTTQSPEDCFKKDGLVKRCMGVTVTLNQARSGFDIS 124
Db 60 PQGDEDDPTPKVPRVFKETVCSKASQQLPEQCAFKEQGVVKQCMGTVTTLNRAAESFDIS 119

Qy 125 CDKDN-----KRFALLGDFPRKSKKEKIGKFKRIVQRIKDFLRNLVPRTE 169
Db 120 CDAPGDFPRFKKISRLAGLLRKGKGFGEKLRIGQIKDFQKLAPEIE 170

RESULT 10
O62840 HORSE PRELIMINARY; PRT; 156 AA.
AC O62840;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Myeloid cathelicidin 1 precursor.
GN Name=cATH-1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
RA Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
RA Zanetti M.;
RT "Novel cathelicidins in horse leukocytes.";
RL FEBS Lett. 457:459-464(1999).
DR EMBL; AJ224927; CAAL12226.1; -; mRNA.
DR HSSP; P32196; 1KWI.
DR SMR; O62840; 30-130.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 156 Potential.
SQ SEQUENCE 156 AA; 17647 MW; BB8EA5D150288FFD CRC64;

Query Match 51.3%; Score 451; DB 2; Length 156;
Best Local Similarity 56.2%; Pred. No. 6e-35;
Matches 95; Conservative 20; Mismatches 32; Indels 22; Gaps 4;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPALAIQAQLSYKEAVLRADIGNORSSDANLYRLLD 60
Db 1 METQRTCLGRWSLVLLLLGLGLVTPPA-TTQALSYKEAVLRADIGNORSSDANLYRLLE 59

Qy 61 LDRPRTWDGDDPTPKPVSTFKVETCPRTTQSPEDCFKKDGLVKRCMGVTVTLNQARGS 120
Db 60 LDPLPKGDKSDTTPKPVSTFKVETCPRTTQSPEDCFKKDGLVKRCMGVTVTLNQARGS 119
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Qy 121 FDISCDKN--KRFALLGDFPRKSKKEKIGKFKRIVQRIKDFLRNLVPR 167
Db 120 FVSCGEPQVRKFG-----RLAKSFLR-----WELLPLR 149

RESULT 11
PMP37 PIG STANDARD; PRT; 167 AA.
AC P49932;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Antibacterial peptide PMAP-37 precursor (Myeloid antibacterial peptide 37).
GN Name=PMAP37;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 131-167.
RC TISSUE=Bone marrow;
RX MEDLINE=95255306; PubMed=7737198;
RA Tosi A., Scocchi M., Zanetti M., Storici P., Gennaro R.;
RT "PMAP-37, a novel antibacterial peptide from pig myeloid cells. cDNA cloning, chemical synthesis and activity.";
RL Eur. J. Biochem. 228:941-946(1995).
CC -!- FUNCTION: Exerts antimicrobial activity against both Gram-positive and negative bacteria with minimal inhibitory concentrations ranging over 1-4 micro molar. Its activity appears to be mediated by its ability to damage bacterial membranes.
CC -!- SIMILARITY: Belongs to the cathelicidin family.

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EMBL; L39641; AAA63447.1; -; mRNA.
PIR; S68967; S68967.
HSSP; P32196; 1KWI.
SMR; P49932; 30-130.
InterPro; IPR001894; Cathelicidin.
DR PANTHER; PTHR10206; Cathelicidins; 1.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 130 Potential.
FT PEPTIDE 131 167 Antibacterial peptide PMAP-37.
FT MOD_RES 30 30 Pyrrolidone carboxylic acid (By similarity).
FT DISULFID 85 96 By similarity.
FT DISULFID 107 124 By similarity.
SQ SEQUENCE 167 AA; 18927 MW; 20F2B59566432992 CRC64;

Query Match 50.6%; Score 444.5; DB 1; Length 167;
Best Local Similarity 57.1%; Pred. No. 2.7e-34;
Matches 92; Conservative 26; Mismatches 40; Indels 3; Gaps 2;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVMPALAIQAQLSYKEAVLRADIGNORSSDANLYRLLD 60
Db 1 METQRTCLGRWSLVLLLLGLVTPPA-SQAQLSYREAVLRVDRNLQESSEANLYRLLE 59

Qy 61 LDRPRTWDGDDPTPKPVSTFKVETCPRTTQSPEDCFKKDGLVKRCMGVTVTLNQARGS 120
Db 60 LDQPKADEDDPTPKPVSTFKVETCPRTTQSPEDCFKENGVRKQCVGTVTLQDKDP 119
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PMP36_PIG

RP NUCLEOTIDE SEQUENCE AND SYNTHESIS OF 130-166

-1- FUNCTION: Exerts antimicrobial activity against both Gram-positive

-!- SIMILARITY: Belongs to the cathelicidin family.

 This entry is correct. It is needed through collection.

CC
DR EMBL; L29125; AAA31070.1; -; mRNA.

UR PIR; S4I/3I; S4I/3I
DR HCSP; P33196; 1KWT

DR HSP; P32196; 1KWL.
DR SMP; P49937; 30-130

DR SMR; P49931; 30-130
DR InterPro: IPR001894

DR INTERPRO; IPR001894
DR DANTYER; DMT10205

DR PANTHER; PTHR10206;
Pform: PTHR10206; Cat:

DR Pram; PF00666; Cath

DR Prodrom; PD001838; C

DR PROSITE; PS00946; C

DR PROSITE; PS00947; C

KW Antibiotic; Antimic

FT	SIGNAL	1
1	1	1

FT PROPER 30

130 PEPTIDE

LT	EFF TIDE	130
FT	MOD RES	30

FT	MOD_KES	30
FT		

FT DTG:FTD 85

FI	DISULFID	83
FT	DISULFID	107

US
FI
SCIENCE
107
166 AB:

SEQUENCE 166 AA;

Q: What's the match?

Query Match

Best Local Similarity

Matches 95; Conserv

1

Qy 1 MKTQRDGHSL

..

Db 1 METQRASLCL

Qy 61 LDPRPTMDGD

Db 60 LDQPPKADED

Qy 121 FDISCDKDNK

Figure 1

三

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rnp) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:45:19 ; Search time 26.3469 Seconds
(Without alignments)
533.455 Million cell updates/sec

Title: US-10-815-562-2

Perfect score: 879

Sequence: 1 MKTQDGHSLGRWSLVLLLL.....KRIIVQIKDFLNLVPTRES 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgm2_6/ptodata/1/iaa/5 COMB.pep:*
2: /cgm2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgm2_6/ptodata/1/iaa/H COMB.pep:*
4: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pep:*
5: /cgm2_6/ptodata/1/iaa/RE COMB.pep:*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	879	100.0	170	1	US-08-313-681A-2
2	879	100.0	170	2	US-09-322-911-2
3	874	99.4	170	2	US-09-917-340-32
4	761	86.6	152	2	US-09-513-999C-7862
5	465.5	53.0	171	1	US-08-313-681A-4
6	465.5	53.0	171	2	US-09-322-911-4
7	457.5	52.0	170	2	US-09-917-340-33
8	451	51.3	156	2	US-09-917-340-35
9	432	49.1	159	2	US-09-917-340-34
10	427.5	48.6	155	2	US-09-917-340-29
11	418.5	47.6	147	1	US-08-243-879A-38
12	418.5	47.6	147	1	US-08-499-523-4
13	418.5	47.6	147	2	US-09-128-345-4
14	418.5	47.6	149	1	US-08-243-879A-36
15	418.5	47.6	149	1	US-08-243-879A-40
16	418.5	47.6	149	1	US-08-243-879A-42
17	418.5	47.6	149	1	US-08-499-523-2
18	418.5	47.6	149	1	US-08-499-523-6
19	418.5	47.6	149	1	US-08-499-523-8
20	418.5	47.6	149	1	US-08-499-523-10
21	418.5	47.6	149	2	US-09-128-345-2
22	418.5	47.6	149	2	US-09-128-345-6
23	418.5	47.6	149	2	US-09-128-345-8
24	418.5	47.6	149	2	US-09-128-345-10
25	415.5	47.3	147	2	US-09-385-328-4
26	415.5	47.3	149	2	US-09-385-328-2
27	415.5	47.3	149	2	US-09-385-328-6

28 415.5 47.3 149 2 US-09-385-328-8 Sequence 8, Appli
29 412 46.9 160 2 US-09-917-340-36 Sequence 36, Appl
30 410.5 46.7 176 2 US-09-917-340-28 Sequence 26, Appl
31 333 37.9 78 2 US-09-513-999C-4349 Sequence 4349, Ap
32 325 37.0 96 1 US-08-313-681A-5 Sequence 5, Appli
33 325 37.0 96 2 US-09-322-911-5 Sequence 5, Appli
34 314 35.7 59 2 US-09-621-976-7180 Sequence 7180, Ap
35 203.5 23.2 66 2 US-09-385-328-17 Sequence 17, Appl
36 197.5 22.5 66 2 US-09-385-328-10 Sequence 10, Appl
37 161 18.3 37 1 US-08-313-681A-6 Sequence 6, Appli
38 161 18.3 37 2 US-09-322-911-6 Sequence 6, Appli
39 154 17.5 36 2 US-09-385-328-11 Sequence 11, Appli
40 133 15.1 27 2 US-09-276-202-8 Sequence 8, Appli
41 125 14.2 27 2 US-09-276-202-2 Sequence 2, Appli
42 118 13.4 27 2 US-09-276-202-3 Sequence 3, Appli
43 117 13.3 24 2 US-09-276-202-10 Sequence 10, Appli
44 117 13.3 27 2 US-09-276-202-4 Sequence 4, Appli
45 113 12.9 23 2 US-09-276-202-11 Sequence 11, Appli

ALIGNMENTS

RESULT 1

US-08-313-681A-2

; Sequence 2, Application US/08313681A

; Patent No. 5618675

; GENERAL INFORMATION:

; APPLICANT: Larrick, James W.

; APPLICANT: Wright, Susan C.

; APPLICANT: Hirata, Mishimasa

; TITLE OF INVENTION: Human Cationic Proteins Having

; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313.681A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.

; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 15325-9-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-313-681A-2

Query Match

Best Local Similarity 100.0%; Score 879; DB 1; Length 170;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTQDGHSLGRWSLVLLLLGLVMP L A I A Q V L S Y K E A V L R A I D G I N Q R S S D A N I Y R L L D 60

Db 1 MKTQDGHSLGRWSLVLLLLGLVMP L A I A Q V L S Y K E A V L R A I D G I N Q R S S D A N I Y R L L D 60

Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Db 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Qy 121 FDISCDKDKRKFALLGDFFRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170
Db 121 FDISCDKDKRKFALLGDFFRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170

RESULT 2
US-09-322-911-2
; Sequence 2, Application US/09322911
; Patent No. 6103888
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; APPLICANT: Balint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09322,911
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,280
; FILING DATE: August 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,761
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,765
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06731
; FILING DATE: July 15, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/313,681
; FILING DATE: September 27, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fittle, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 15325-000920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-322-911-2

Query Match 100.0%; Score 879; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Db 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Qy 121 FDISCDKDKRKFALLGDFFRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170
Db 121 FDISCDKDKRKFALLGDFFRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170

RESULT 3
US-09-917-340-32
; Sequence 32, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TELANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-32

Query Match 99.4%; Score 874; DB 2; Length 170;
Best Local Similarity 99.4%; Pred. No. 4.3e-95;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Db 61 LDRPTMDGDDPTPKPVSFTVKETVCPRTTQOSPEDCDFKDGLVKRCMGVTTLNQARGS 120
Qy 121 FDISCDKDKRKFALLGDFFRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170
Db 121 FDISCDKDKRKFALLGDFFRKSKGKIGKFKRIVQRIKDFLNLVPRTES 170

RESULT 4
US-09-513-999C-7862
; Sequence 7862, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm

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; SEQ ID NO 7862
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -33...-1
; OTHER INFORMATION: score 9.5
; OTHER INFORMATION: seq LLLGLVPLAIIA/QV
US-09-513-999C-7862

Query Match      86.6%; Score 761; DB 2; Length 152;
Best Local Similarity 98.6%; Pred. No. 8.2e-82;
Matches 146; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTORDGHSGLRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 4 MKTORDGHSGLRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 63
QY 61 LDPRTMDGDDPTPKVSVTVKTCVPRTTQSPEDCDPKDGLVKRCMGTVTTLNQARGS 120
Db 64 LDPRTMDGDDPTPKVSVTVKTCVPRTTQSPEDCDPKDGLVKRCMGTVTTLNQARGS 123
QY 121 FDISCDKDKRFPALLGDFPRKSKKIGK 148
Db 124 FDISCDKDKRFPALLGDFPRKSKKMAK 151

RESULT 5
US-08-313-681A-4
; Sequence 4, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; TITLE OF INVENTION: Human Cationic Proteins Having
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,681A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15325-9-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-313-681A-4

Query Match      53.0%; Score 465.5; DB 1; Length 171;
Best Local Similarity 57.3%; Pred. No. 8e-47;

Matches 98; Conservative 26; Mismatches 44; Indels 3; Gaps 2;

QY 1 MKTORDGHSGLRWSLVLLLLGLVPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 METHKHGPSLAWWSLLLLGLLMPPA-IAQDLTYREAVLRAVDAPNQSSSEANLYRLLS 59
QY 61 LDPRTMDGDDPTPKVSVTVKTCVPRTTQSPEDCDPKDGLVKRCMGTVTTLNQARGS 120
Db 60 MDPQLEDAKPYTPQVSVTVKTCVPRTTQSPEDCDPKDGLVKRCMGTVTTRYQAWDS 119
QY 121 FDISCDK--DNKRFPALLGDFPRKSKKIGKPKRIVQRIKDFLRNLVPRTE 169
Db 120 FDIRCNRAQESPEPTGLRKRLKPKFNKKEKLLKXKQKLGKLLPKLAPRTD 170

RESULT 6
US-09-322-911-4
; Sequence 4, Application US/09322911
; Patent No. 6103888
; GENERAL INFORMATION:
; APPLICANT: Larrick, James W.
; APPLICANT: Wright, Susan C.
; APPLICANT: Hirata, Mishimasa
; APPLICANT: Balint, Robert F.
; TITLE OF INVENTION: Human Cationic Proteins Having
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,911
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,280
; FILING DATE: August 1, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,761
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,765
; FILING DATE: July 17, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06731
; FILING DATE: July 15, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/313,681
; FILING DATE: September 27, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 15325-000920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-322-911-4
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; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Equus asinus
US-09-917-340-35

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1	QY	1	MKTORDGHSIGRSLVLLGLGLVWPLAI	IAQVLSYKEAVLRADIGINQRSSDANLYRLD	60
			: : : : :	: : : : :	
			: : : : :	: : : : :	
1	Db	1	METQRTNRCIGRWSPLLLGLVPPA	TTQALSYKEAVLRADIGINQRSSDENLYRLLE	59
			: : : : :	: : : : :	
			: : : : :	: : : : :	
61	QY	61	LDRPRTWDGDDPTPKPVSFTVTKETV	CPRTTQQSPEDCDFKDGVLKRCMGTVTLNQARGS	120
			: : : : :	: : : : :	
60	Db	60	LDLPLPKGDKDSPTPKPVSFVTKETV	CPRIKMQTPEQCDFKENGVLKQCVTVILGPFVKDH	119
			: : : : :	: : : : :	
			: : : : :	: : : : :	
121	QY	121	FDLSCDKDN--KRFALLGDFFRKSKEK	IGFKRIVQRIKDFLNLVPR	167
			: : : : :	: : : : :	
			: : : : :	: : : : :	
120	Db	120	FDVSCGEPORVKRFG	-----RLAKSFRL-----	MLLAPR 149
			: : : : :	: : : : :	
			: : : : :	: : : : :	

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/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: 60/249,602
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: 60/290,932
/ PRIOR FILING DATE: 2001-05-15
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 34
/ LENGTH: 159
/ TYPE: PRT
/ ORGANISM: Bos taurus
US-09-917-340-34

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Qy	1	MTKTRDCHSLGRSLVLLLLGLVMPPLAI	IAQVLSYKEAVLR	RAIDGINORSSDANLYRLLD	60
Db	1	METQRASLSLGRSLVLLLLGLALPSA	SAQALSRYEAVLR	FAVDQLNEKSSSEANLYRLLE	59
Qy	61	LDRPRPTWDGP	PPTPKVSVTVK	ETVCPRTTQOSPEDCFKCDGLVKECGVTVLNQARG	119
Db	60	LDPFPKEDDENPNI	PKPVSFRVKE	TVCPRTSQSPQPCDFAKENGLLKECVGTIVLDQVGS	119
Qy	120	SFDISC	125		
Db	120	NFDITC	125		


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; TEL: (202) 887-1500
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-243-879A-38

Query Match          47.6%; Score 418.5; DB 1; Length 147;
Best Local Similarity 65.4%; Pred. No. 2.3e-41;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1

QY 1 MKTORGHSLGRWSLVLLGLVMPPLAIIAQLVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 METPRASLCLGRWSLVLLGLLALVPSA-SAQALSRYEAVLRAVDRLNEQSSEANLYRLLE 59

QY 61 LDPRPTMDGDDPTPKVSVFTVKETVCPRTTQOSPBCDFKKGDLVKRCMGTVTLNQARG 120
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 LDQPPKADEDGPTPKVSVFTVKETVCPRTTQPPQCDPKENGLKRCCEGTVTLDOVRGN 119

QY 121 FDISCDK 127
   |||:
Db 120 LDITCNE 126

RESULT 12
US-08-499-523-4
; Sequence 4, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARMIG, SYLVIA S.L.
; APPLICANT: KOKRYAKOV, VLADIMIR N.
; TITLE OF INVENTION: PROTEGRINS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/499,523
; FILING DATE: 07-JUL-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.24
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-499-523-4

Query Match          47.6%; Score 418.5; DB 1; Length 147;
Best Local Similarity 65.4%; Pred. No. 2.3e-41;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1

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QY 1 MKTORDGHSICGRWSLVLLGLVMPPLATIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 Db 1 METQRASICLGRWSLWLLLLALVWPSA-SAQALSSTREAVLRAVDRLNEQSSSEANLYRLLE 59
 QY 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
 Db 60 LDQPPKADEDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 119
 QY 121 FDISCDK 127
 Db 120 LDITCNE 126

RESULT 13
 US-09-128-345-4
 ; Sequence 4, Application US/09128345
 ; Patent No. 6159936
 ; GENERAL INFORMATION:
 ; APPLICANT: LEHRER, ROBERT I.
 ; APPLICANT: HARWIG, SYLVIA S.L.
 ; APPLICANT: KORYAKOV, VLADIMIR N.
 ; TITLE OF INVENTION: PROTEGRINS
 ; NUMBER OF SEQUENCES: 76
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/128,345
 ; FILING DATE: 03-AUG-1998
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura, A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 8067-0054-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 147 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-128-345-4

Query Match 47.6%; Score 418.5; DB 2; Length 147;
 Best Local Similarity 65.4%; Pred. No. 2.3e-41;
 Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
 QY 1 MKTORDGHSICGRWSLVLLGLVMPPLATIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 Db 1 METQRASICLGRWSLWLLLLALVWPSA-SAQALSSTREAVLRAVDRLNEQSSSEANLYRLLE 59
 QY 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
 Db 60 LDQPPKADEDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 119
 QY 121 FDISCDK 127
 Db 120 LDITCNE 126

RESULT 14
 US-08-243-879A-36
 ; Sequence 36, Application US/08243879A
 ; Patent No. 5708145
 ; GENERAL INFORMATION:
 ; APPLICANT: LEHRER, ROBERT I.
 ; APPLICANT: HARWIG, SYLVIA S.L.
 ; TITLE OF INVENTION: A NEW PROTEGRIN
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
 ; CITY: Washington, DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/243,879A
 ; FILING DATE: 17-MAY-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 2000-0540.22
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 887-1500
 ; TELEFAX: (202) 887-0763
 ; TELEX: 90-4030
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 149 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-243-879A-36

Query Match 47.6%; Score 418.5; DB 1; Length 149;
 Best Local Similarity 65.4%; Pred. No. 2.3e-41;
 Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
 QY 1 MKTORDGHSICGRWSLVLLGLVMPPLATIAQVLSYKEAVLRAIDGINORSSDANLYRLLD 60
 Db 1 METQRASICLGRWSLWLLLLALVWPSA-SAQALSSTREAVLRAVDRLNEQSSSEANLYRLLE 59
 QY 61 LDPRTMDGDDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 120
 Db 60 LDQPPKADEDPTPKPVSTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLLNQARGS 119
 QY 121 FDISCDK 127
 Db 120 LDITCNE 126

RESULT 15
 US-08-243-879A-40
 ; Sequence 40, Application US/08243879A
 ; Patent No. 5708145
 ; GENERAL INFORMATION:
 ; APPLICANT: LEHRER, ROBERT I.
 ; APPLICANT: HARWIG, SYLVIA S.L.
 ; TITLE OF INVENTION: A NEW PROTEGRIN
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
 ; CITY: Washington, DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,879A
; FILING DATE: 17-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0540.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-243-879A-40

Query Match      47.6%; Score 418.5; DB 1; Length 149;
Best Local Similarity 65.4%; Pred. No. 2.3e-41;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

Qy      1 MKTORGHSLGRWSLVALLGLVMPLEIIAQVLVSYKEAVLRALDGINORSSDANLYRLLD 60
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Db      1 METQASLCGLGRWSLWLLLLALVPSA-SAQAISYREAVLRADRLNEQSSEANLYRLLE 59
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy      61 LDPRTMDGDPDTPKPVSVFTVKETVCPRTTQSPEDCDPKDGLVKRCMGTVTLNQARGS 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      60 LDQPPKADEDGTPKPVSVFTVKETVCPRTTRQPPPELCPDKENGVRVKQCVGTITLDQIKDP 119
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy      121 FDISCDK 127
      ||| |||
Db      120 LDITCNE 126
      ||| |||

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Search completed: January 12, 2006, 21:51:59
Job time : 26.3469 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:45:40 ; Search time 70.2583 Seconds
(without alignments)
1010.998 Million cell updates/sec

Title: US-10-815-562-2
Perfect score: 879
Sequence: 1 MKTQDGHSLGRWSLVLLLL.....KRIVQIKDFLNLVPRTES 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	879	100.0	170	4	US-10-603-566-51
2	879	100.0	170	5	US-10-893-485-51
3	874	99.4	170	3	US-09-917-340-32
4	874	99.4	170	5	US-10-844-837-32
5	874	99.4	170	5	US-10-777-683-4
6	874	99.4	170	5	US-10-909-119-47
7	874	99.4	170	5	US-10-657-851-32
8	874	99.4	170	5	US-10-287-436A-513
9	874	99.4	170	5	US-10-287-436A-1204
10	865	98.4	170	4	US-10-344-709C-11
11	468.5	53.3	171	4	US-10-344-709C-7
12	457.5	52.0	170	3	US-09-917-340-33
13	457.5	52.0	170	5	US-10-844-837-33
14	457.5	52.0	170	5	US-10-909-119-48
15	457.5	52.0	170	5	US-10-657-851-33
16	451	51.3	156	3	US-09-917-340-35
17	451	51.3	156	5	US-10-844-837-35
18	451	51.3	156	5	US-10-909-119-50
19	451	51.3	156	5	US-10-657-851-35
20	432	49.1	159	3	US-09-917-340-34
21	432	49.1	159	5	US-10-844-837-34
22	432	49.1	159	5	US-10-909-119-49
23	432	49.1	159	5	US-10-657-851-34
24	431.5	49.1	173	4	US-10-344-709C-5
25	427.5	48.6	155	3	US-09-917-340-29
26	427.5	48.6	155	4	US-10-344-709C-8
27	427.5	48.6	155	5	US-10-844-837-29

28	427.5	48.6	155	5	US-10-909-119-44	Sequence 44, Appl
29	427.5	48.6	155	5	US-10-657-851-29	Sequence 29, Appl
30	418.5	47.6	147	3	US-09-539-443-4	Sequence 4, Appl
31	418.5	47.6	147	4	US-10-627-829-4	Sequence 4, Appl
32	418.5	47.6	149	3	US-09-539-443-2	Sequence 2, Appl
33	418.5	47.6	149	3	US-09-539-443-6	Sequence 6, Appl
34	418.5	47.6	149	3	US-09-539-443-8	Sequence 8, Appl
35	418.5	47.6	149	3	US-09-539-443-10	Sequence 10, Appl
36	418.5	47.6	149	4	US-10-627-829-2	Sequence 2, Appl
37	418.5	47.6	149	4	US-10-627-829-6	Sequence 6, Appl
38	418.5	47.6	149	4	US-10-627-829-8	Sequence 8, Appl
39	418.5	47.6	149	4	US-10-627-829-10	Sequence 10, Appl
40	413	47.0	158	5	US-10-485-278-8	Sequence 8, Appl
41	412	46.9	160	3	US-09-917-340-36	Sequence 36, Appl
42	412	46.9	160	5	US-10-844-837-36	Sequence 36, Appl
43	412	46.9	160	5	US-10-909-119-51	Sequence 51, Appl
44	412	46.9	160	5	US-10-657-851-36	Sequence 36, Appl
45	410.5	46.7	176	3	US-09-917-340-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-10-603-566-51
; Sequence 51, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandembogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-51

Query Match	100.0%	Score 879;	DB 4;	Length 170;
Best Local Similarity	100.0%	Pred. No. 1.7e-87;		
Matches	170;	Conservative	0;	Mismatches
			0;	Gaps
Qy	1	MKTQDGHSLGRWSLVLLLLGLVMPFLAI	IAQVLSYKEAVLRAIDGINQRSSDANLYRLLD	60
Db	1	MKTQDGHSLGRWSLVLLLLGLVMPFLAI	IAQVLSYKEAVLRAIDGINQRSSDANLYRLLD	60
Qy	61	LDPRPTMGDDPTPKPVSTTKETVCPRTTQOSPEDCDPKKGLVKRCMGTVTLLNQARGS	120	
Db	61	LDPRPTMGDDPTPKPVSTTKETVCPRTTQOSPEDCDPKKGLVKRCMGTVTLLNQARGS	120	
Qy	121	FDISCDKDKRFPALLGDFPRKSKKIKGFKRIQRIKDFLNLVPRTES	170	
Db	121	FDISCDKDKRFPALLGDFPRKSKKIKGFKRIQRIKDFLNLVPRTES	170	

RESULT 2

US-10-893-485-51
; Sequence 51, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:

APPLICANT: Wittamer, Valerie
APPLICANT: Communi, David
APPLICANT: Vandenberg, Ann
APPLICANT: Dethoux, Michel
APPLICANT: Parmentier, Marc
TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
CURRENT APPLICATION NUMBER: US/10/893,485
CURRENT FILING DATE: 2004-07-16
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US10/603,858
PRIOR FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: US 09/905,253
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 10/201,187
PRIOR FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-10-893-485-51

Query Match 100.0%; Score 879; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.7e-87;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDPRTMDGDDTPKPVSTTKVETVCPRTTQOSPEDCDFKDGVLKRCMGTVTTLNQARGS 120
Db 61 LDPRTMDGDDTPKPVSTTKVETVCPRTTQOSPEDCDFKDGVLKRCMGTVTTLNQARGS 120
Qy 121 FDISCDKDKRFPALLGDPFRKSKGKIGKEFKRIVQRIKDFLRNLVPRTES 170
Db 121 FDISCDKDKRFPALLGDPFRKSKGKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 3
US-09-917-340-32
Sequence 32, Application US/09917340
Patent No. US20020090369A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-32

Query Match 99.4%; Score 874; DB 3; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60

Db 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDPRTMDGDDTPKPVSTTKVETVCPRTTQOSPEDCDFKDGVLKRCMGTVTTLNQARGS 120
Db 61 LDPRTMDGDDTPKPVSTTKVETVCPRTTQOSPEDCDFKDGVLKRCMGTVTTLNQARGS 120
Qy 121 FDISCDKDKRFPALLGDPFRKSKGKIGKEFKRIVQRIKDFLRNLVPRTES 170
Db 121 FDISCDKDKRFPALLGDPFRKSKGKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 4
US-10-844-837-32
Sequence 32, Application US/10844837
Publication No. US20050014932A1
GENERAL INFORMATION:
APPLICANT: Imboden, Michael
APPLICANT: Homan, Jane
APPLICANT: Bremel, Robert D.
TITLE OF INVENTION: Targeted Biocides
FILE REFERENCE: IOGEN-09014
CURRENT APPLICATION NUMBER: US/10/844,837
CURRENT FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-10-844-837-32

Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRDGHSLGRWSLVLLLLGLVMPALIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDPRTMDGDDTPKPVSTTKVETVCPRTTQOSPEDCDFKDGVLKRCMGTVTTLNQARGS 120
Db 61 LDPRTMDGDDTPKPVSTTKVETVCPRTTQOSPEDCDFKDGVLKRCMGTVTTLNQARGS 120
Qy 121 FDISCDKDKRFPALLGDPFRKSKGKIGKEFKRIVQRIKDFLRNLVPRTES 170
Db 121 FDISCDKDKRFPALLGDPFRKSKGKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 5
US-10-777-683-4
Sequence 4, Application US/10777683
Publication No. US20050032117A1
GENERAL INFORMATION:
APPLICANT: Richard B. Moss
APPLICANT: Akitoashi Ishizaka
APPLICANT: Teruo Kiriaka
TITLE OF INVENTION: Method for Assessment of Cystic Lung Fibrosis
FILE REFERENCE: Q74236
CURRENT APPLICATION NUMBER: US/10/777,683
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: US 60/447,310
PRIOR FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-10-777-683-4

Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;

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Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTORDGHSGLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRNGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
Db 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
Qy 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
Db 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 6
US-10-909-119-47
; Sequence 47, Application US/10909119
; Publication No. US20050079578A1
; GENERAL INFORMATION:
; APPLICANT: Centanni, John M.
; TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
; FILE REFERENCE: STRATA-09123
; CURRENT APPLICATION NUMBER: US/10/909,119
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-119-47

Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTORDGHSGLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRNGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
Db 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
Qy 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
Db 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 7
US-10-657-851-32
; Sequence 32, Application US/10657851
; Publication No. US20050089836A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAulity, Jonathan P.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/10/657,851
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/917,340
; PRIOR FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 32
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-851-32

Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTORDGHSGLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRNGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
Db 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
Qy 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
Db 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 8
US-10-287-436A-513
; Sequence 513, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-513

Query Match 99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKTORDGHSGLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Db 1 MKTQRNGHSLGRWSLVLLLLGLVMPALIAIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
Qy 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
Db 61 LDPRTMDGDDPTPKVSVFTVKETVCPRTTQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
Qy 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170
Db 121 FDISCDKDKRFPALLGDFPRKSKKIGKEFKRIVQRIKDFLRNLVPRTES 170

RESULT 9
US-10-287-436A-1204
; Sequence 1204, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; SOFTWARE: PatentIn Ver. 2.0
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Db      60  LDLPKDGKDSITPKVPSPVFKETVCPRIIMKQTPQEQCDPKENGVLKQCVGTWILDPMVKDY 119
QY      121  PDISCDKN--KRFALLGDFFRKSKKIGKEPK-----RIVQRIK 158
Db      120  PDASCDQPKVRKTHSVGLSLTQRMQIRKDKSEATHRGIRIITRPK 165

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RESULT 15
US-10-657-851-33
; Sequence 33, Application US/10657851
; Publication No. US2005008936A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/10/657,851
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/917,340
; PRIOR FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 33
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-657-851-33

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; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Equus caballus
; US-10-657-851-33

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Best Local Similarity 57.2%; Pred. No. 1.8e-41;
Matches 95; Conservative 24; Mismatches 38; Indels 9; Gaps 3;

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Db      1  METQRTCLGRWSPLVLLGLVPPA-TTQALS YKEAVLRAVDGLNQRSSDENLYRLLE 59
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      61  LDRPRTWGDGDDTPKPSVFTVKTVCPTTQQSPEDCDPKKQGLVKRCMGTTVLNQARGS 120
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      60  LDPLPKGDKSDTPKPSFWVKETVCPRIMKQTPQCDPKENGVLVKCVGTVIDLPVKDY 119
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      121  FDISCDKN--KRPALLGDFFRSKEKIGKEPK-----RIVQRIK 158
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      120  FDISCDPEQRVKGFHSVGSGLIQRHQIMRDKSATRHGIRIITRPK 165
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[illegible]

Query Match	52.0%	Score	457.5;	DB	5;	Length	170;
Best Local Similarity	57.2%;	Pred.	No.1.8e-41;				
Matches	95;	Conservative	24;	Mismatches	38;	Indels	9; Gaps 3;
Qy	1	MKTORDGHSIGRWSLVLLGLGLMPLAIILAAVLTSYKEAVLRADGINQRSSDANLYRLLD	60				
	:	: :	:	:	:	:	:
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
Dd	1	METQRNTRCLGRWSPLLLLLLGLVTPPPA-TTQAUSYKEAVLRADGLNQRSSDENLYRLL	59				
	:	:	:	:	:	:	:
Qy	61	LDRPRITMDGDPDTPKPSVFYTKETVCVRPTTQQSPEDCDFFKKDGLVKRCMGVTIVLNQARGS	120				
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:
	:	:	:	:	:	:	:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2006, 21:48:15 ; Search time 7.52768 Seconds
(without alignments)
213.508 Million cell updates/sec

Title: US-10-815-562-2

Perfect score: 879

Sequence: 1 MKTQDGHSLGRWSLVLLLL.....KRIVQRKDFLRNLVPTRES 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	21.0	37	US-10-985-426-9	Sequence 9, Appli
2	76.5	8.7	491	US-10-793-626-406	Sequence 406, App
3	76.5	8.7	491	US-10-793-626-2104	Sequence 2104, Ap
4	70.5	8.0	867	US-10-131-826A-20	Sequence 20, Appl
5	70.5	8.0	870	US-10-933-025-6	Sequence 6, Appli
6	70.5	8.0	870	US-10-933-025-15	Sequence 15, Appl
7	70	8.0	645	US-10-821-234-1409	Sequence 1409, Ap
8	64.5	7.3	693	US-11-196-475-68	Sequence 68, Appl
9	63	7.2	325	US-11-052-554A-356	Sequence 356, App
10	63	7.2	1717	US-11-192-967-2	Sequence 2, Appli
11	63	7.2	1717	US-11-193-715-2	Sequence 8, Appli
12	62.5	7.1	874	US-11-012-762-8	Sequence 198, App
13	62	7.1	192	US-11-033-365-198	Sequence 200, App
14	62	7.1	301	US-11-033-365-200	Sequence 362, App
15	62	7.1	301	US-11-074-176-362	Sequence 254, App
16	62	7.1	308	US-11-074-176-254	Sequence 20, Appl
17	62	7.1	383	US-10-517-939-20	Sequence 347, App
18	62	7.1	1061	US-11-000-463-347	Sequence 348, App
19	62	7.1	1091	US-11-000-463-348	Sequence 15, Appl
20	61.5	7.0	236	US-11-100-183-15	Sequence 17, Appl
21	61.5	7.0	240	US-11-100-183-17	Sequence 1950, Ap
22	61.5	7.0	439	US-10-467-657-1990	Sequence 134, App
23	61.5	7.0	1189	US-11-074-176-134	Sequence 1002, App
24	61.5	7.0	4495	US-10-453-372-1002	Sequence 42, Appl
25	60.5	6.9	148	US-11-174-150-42	

26 60.5 6.9 275 6 US-10-821-234-1013 Sequence 1013, Ap
27 60.5 6.9 748 6 US-10-467-657-8036 Sequence 8036, Ap
28 60.5 6.9 1166 6 US-10-821-234-964 Sequence 964, App
29 60.5 6.9 1466 7 US-11-186-284-33 Sequence 33, Appl
30 60.5 6.9 1627 6 US-10-821-234-1283 Sequence 1283, Ap
31 60.5 6.9 3690 6 US-10-995-561-1016 Sequence 1016, Ap
32 60.5 6.9 3714 6 US-10-995-561-1015 Sequence 1015, Ap
33 60.5 6.9 3717 6 US-10-821-234-1076 Sequence 1076, Ap
34 60 6.8 191 7 US-11-033-365-160 Sequence 160, App
35 60 6.8 192 7 US-11-033-365-159 Sequence 159, App
36 60 6.8 192 7 US-11-033-365-197 Sequence 197, App
37 60 6.8 192 7 US-11-187-522-1 Sequence 1, Appl
38 60 6.8 193 7 US-11-033-365-196 Sequence 196, App
39 60 6.8 196 7 US-11-033-365-199 Sequence 199, App
40 60 6.8 202 7 US-11-144-889A-2 Sequence 2, Appl
41 60 6.8 241 7 US-11-100-183-19 Sequence 19, Appl
42 60 6.8 286 6 US-10-954-468-25 Sequence 25, Appl
43 60 6.8 287 6 US-10-954-468-17 Sequence 17, Appl
44 60 6.8 287 6 US-10-954-468-24 Sequence 24, Appl
45 60 6.8 288 6 US-10-954-468-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-10-985-426-9
; Sequence 9, Application US/10985426
; Publication No. US20050256069A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottathil G.
; TITLE OF INVENTION: IRNA AGENTS WITH BIOCLEAVABLE TETHERS
; FILE REFERENCE: 14174-099001
; CURRENT APPLICATION NUMBER: US/10/985,426
; PRIORITY FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 10/916,185
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US2004/011829
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/465,665
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/463,772
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/469,612
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/465,802
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/493,986
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 60/494,597
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 60/503,414
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/506,341
; PRIOR FILING DATE: 2003-09-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary Cell Permeation Peptides
US-10-985-426-9

Query Match 21.0%; Score 185; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.2e-14;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 LLGDFPKSKKIKGPKRIVQRKDFLRNLVPTRES 170
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Db 1 LIGDFFRKSKKIGKEFKRIIVQRIKDFLRNLVPTES 37

RESULT 2

US-10-793-626-406
; Sequence 406, Application US/10793626
; Publication No. US20050255478A1

GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 406
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-406

Query Match 8.7%; Score 76.5; DB 6; Length 491;
Best Local Similarity 21.3%; Pred. No. 0.91; Mismatches 65; Indels 27; Gaps 5;
Matches 33; Conservative 30

Qy 13 WSLVLLGLVMPALIAQV----LSYKEAVLRAIDGINORSSDANL-----YRLDLD 62

Db 32 WHFILVILGILTSIITVSTILSHQK-----GLN-KEQRLNKKIEVYVQTINKD 84

Qy 63 PRPTMGDPDPKPVSVFTVETVCPRTTQQSPEDCFKKGLVKRCMGTVTTLNQARGSFD 122

Db 85 YYKQSSDKLTQSAIDGMVKELKDPYSEYMTABETKQFNEGVSDFVG-----IG 134

Qy 123 ISCDKDKRFPALLGDFFRKSKKEKIKPKRIVQRI 157

Db 135 AEMQKNEQISVTPMKDSPAERKAGIQPKDITVQV 169

RESULT 3

US-10-793-626-2104
; Sequence 2104, Application US/10793626
; Publication No. US20050255478A1

GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2104
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2104

Query Match 8.7%; Score 76.5; DB 6; Length 491;
Best Local Similarity 21.3%; Pred. No. 0.91; Mismatches 65; Indels 27; Gaps 5;
Matches 33; Conservative 30

Qy 13 WSLVLLGLVMPALIAQV----LSYKEAVLRAIDGINORSSDANL-----YRLDLD 62

Db 32 WHFILVILGILTSIITVSTILSHQK-----GLN-KEQRLNKKIEVYVQTINKD 84

Qy 63 PRPTMGDPDPKPVSVFTVETVCPRTTQQSPEDCFKKGLVKRCMGTVTTLNQARGSFD 122

Db 85 YYKQSSDKLTQSAIDGMVKELKDPYSEYMTABETKQFNEGVSDFVG-----IG 134

Qy 123 ISCDKDKRFPALLGDFFRKSKKEKIKPKRIVQRI 157

Db 135 AEMQKNEQISVTPMKDSPAERKAGIQPKDITVQV 169

RESULT 4

US-10-131-826A-20
; Sequence 20, Application US/10131826A
; Publication No. US20050245730A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131.826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 20
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-20

Query Match 8.0%; Score 70.5; DB 6; Length 867;
Best Local Similarity 20.4%; Pred. No. 9.1;
Matches 47; Conservative 27; Mismatches 59; Indels 97; Gaps 10;

Qy 3 TORDGHSLGRWSLVLLGLVMPALIAQVLSYKEAVLRAIDGINORSSDANLYRLDLD 62

Db 315 TADGHVHIGQGLV---KKGMPYEFDIRVPFY-----VRGPNVBAAGLNPVILNID 364

```
Qy 63 PRPT-----MDGDP-----DTPKPV-----SPTVK----- 82
Db 365 LAPTILDIAGLDIPADMKGSLKLLDTERPVNRFHLKKGKRVWRDSEFLVGRGKLLHKRD 424
Qy 83 -----ETVCPRTTQ--QSPEDCDFFKXGGLVGRGCMGTVT 113
Db 425 NDKVDAQEENFLPKYQVRKDLQRAEYQTACEQLGQKWCVEDATGKLGK--LHKCKGPMR 482
Qy 114 LNOAR-----GSPDISCDKONKRFALLGDFPRKSKKEKIGKEFK 151
Db 483 LGGSRALSNLVPKYQGGSEACTCDSGDKLSLAG-----RRKGLFKKKYK 528
```

RESULT 5

```
US-10-933-025-6
; Sequence 6, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEFAN
; APPLICANT: HEMMERICH, STEFAN
; TITLE OF INVENTION: Sulfotransferases and methods of use
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025
; CURRENT FILING DATE: 2004-09-01
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2000-12-27
; PRIOR FILING DATE: 2000-12-27
; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-933-025-6
```

```
Query Match 8.0%; Score 70.5; DB 6; Length 870;
Best Local Similarity 20.4%; Pred. No. 9.1;
Matches 47; Conservative 27; Mismatches 59; Indels 97; Gaps 10;

Qy 3 TORGHSLGRWSLVLLGLVPLAITAQVLSYKEAVLRAIDGINQRSSDANLYRLDLD 62
Db 315 TADGHYHIGQGLV---KGKSMPEYFDIRVPFY-----VRGPNVEAGCLNPHIVLND 364
Qy 63 PRPT-----MDGDP-----DTPKPV-----SPTVK----- 82
Db 365 LAPTILDIAGLDIPADMKGSLKLLDTERPVNRFHLKKGKRVWRDSEFLVGRGKLLHKRD 424
Qy 83 -----ETVCPRTTQ--QSPEDCDFFKXGGLVGRGCMGTVT 113
Db 425 NDKVDAQEENFLPKYQVRKDLQRAEYQTACEQLGQKWCVEDATGKLGK--LHKCKGPMR 482
Qy 114 LNOAR-----GSPDISCDKONKRFALLGDFPRKSKKEKIGKEFK 151
Db 483 LGGSRALSNLVPKYQGGSEACTCDSGDKLSLAG-----RRKGLFKKKYK 528
```

RESULT 6

```
US-10-933-025-15
; Sequence 15, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEFAN
; APPLICANT: HEMMERICH, STEFAN
; TITLE OF INVENTION: Sulfotransferases and methods of use
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025
```

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; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: 10/025,966
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/258,577
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/267,831
; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-933-025-15
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```
Query Match 8.0%; Score 70.5; DB 6; Length 870;
Best Local Similarity 20.4%; Pred. No. 9.1;
Matches 47; Conservative 27; Mismatches 59; Indels 97; Gaps 10;

Qy 3 TORGHSLGRWSLVLLGLVPLAITAQVLSYKEAVLRAIDGINQRSSDANLYRLDLD 62
Db 315 TADGHYHIGQGLV---KGKSMPEYFDIRVPFY-----VRGPNVEAGCLNPHIVLND 364
Qy 63 PRPT-----MDGDP-----DTPKPV-----SPTVK----- 82
Db 365 LAPTILDIAGLDIPADMKGSLKLLDTERPVNRFHLKKGKRVWRDSEFLVGRGKLLHKRD 424
Qy 83 -----ETVCPRTTQ--QSPEDCDFFKXGGLVGRGCMGTVT 113
Db 425 NDKVDAQEENFLPKYQVRKDLQRAEYQTACEQLGQKWCVEDATGKLGK--LHKCKGPMR 482
Qy 114 LNOAR-----GSPDISCDKONKRFALLGDFPRKSKKEKIGKEFK 151
Db 483 LGGSRALSNLVPKYQGGSEACTCDSGDKLSLAG-----RRKGLFKKKYK 528
```

RESULT 7

```
US-10-821-234-1409
; Sequence 1409, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PF_SEQ_genes Version 1.0
; SEQ ID NO 1409
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1409
```

```
Query Match 8.0%; Score 70; DB 6; Length 645;
Best Local Similarity 24.0%; Pred. No. 6.8;
Matches 36; Conservative 22; Mismatches 40; Indels 52; Gaps 7;

Qy 15 LVLLGLVPLAITAQVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMGDGDPTP 74
Db 8 LLLGLGLVQLLAV-----AGAEPSDSSN----- 33
Qy 75 KPVSFYKVTVCPRTTQSPEDCDFFKXGGLVGRGCMGTVTLNQARGSPD--ISCDKONKRF 132
Db 34 -----RENAIEDESEEDDEEDDLVKEENGVLVNDL--NFDNFDVADK----- 80
Qy 133 ALLGDFPRK-----SKEKIGKEFKRIVQRIKD 159
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Db 81 TVLLEFYAPWCGCHKQFAPYEKIANILKD 110

RESULT 8

US-11-196-475-68

; Sequence 68, Application US/11196475

; Publication No. US20050271682A1

; GENERAL INFORMATION:

; APPLICANT: Dattwyler, Raymond J.

; APPLICANT: Gomes Solecki, Maria J. C.

; APPLICANT: Luft, Benjamin J.

; APPLICANT: Dunn, John J.

; TITLE OF INVENTION: Recombinant Constructs of Borrelia

; TITLE OF INVENTION: Burgdorferi

; FILE REFERENCE: 2631.1001-011

; CURRENT APPLICATION NUMBER: US/11/196,475

; PRIOR FILING DATE: 2005-08-03

; PRIOR APPLICATION NUMBER: US 08/148,191

; PRIOR FILING DATE: 1993-11-01

; PRIOR APPLICATION NUMBER: US 08/235,836

; PRIOR FILING DATE: 1994-04-29

; PRIOR APPLICATION NUMBER: US 09/666,017

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: US 60/226,484

; PRIOR FILING DATE: 2000-08-18

; PRIOR APPLICATION NUMBER: PCT/US01/24736

; PRIOR FILING DATE: 2001-08-07

; NUMBER OF SEQ ID NOS: 213

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 68

; LENGTH: 693

; TYPE: PRT

; ORGANISM: Borrelia burgdorferi

US-11-196-475-68

Query Match 7.3%; Score 64.5; DB 7; Length 693;

Best Local Similarity 27.1%; Pred. No. 30;

Matches 36; Conservative 21; Mismatches 53; Indels 23; Gaps 7;

Qy 36 KEAVLRAIDGINQRSSDANLYRLDLDPRPTMGDPDPK-PVSVFTVETVCPRTTQSP 94

Db 324 REKIQEDIDEINK-----EKNL-----PKP---GDVSSPKVDKQLQIKESLEDLQELKE 370

Qy 95 EDCDFKQGLVKRCMGTVTLNQARSGFDISCDKDKRALLGDFPK--SKEKI-GKEFK 151

Db 371 TSDENQKREIEKQ-----IBIKSDBELLKSKOPKALDNLNGLSKRVSSKEKIKGKEGE 424

Qy 152 RIVQRIKDFLRNL 164

Db 425 IVKESKASLADL 437

RESULT 9

US-11-052-554A-356

; Sequence 356, Application US/11052554A

; Publication No. US20050289866A1

; GENERAL INFORMATION:

; APPLICANT: Sachdeva, et al.

; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

; FILE REFERENCE: 30853/40359A

; CURRENT APPLICATION NUMBER: US/11/052,554A

; CURRENT FILING DATE: 2005-02-07

; PRIOR APPLICATION NUMBER: US 60/589,227

; PRIOR FILING DATE: 2004-07-20

; PRIOR APPLICATION NUMBER: IN 173/DEL/2004

; PRIOR FILING DATE: 2004-02-06

; NUMBER OF SEQ ID NOS: 763

; SOFTWARE: Patent version 3.3

; SEQ ID NO 356

; LENGTH: 325

; TYPE: PRT

; ORGANISM: Streptococcus mutans UA159

US-11-052-554A-356

Query Match 7.2%; Score 63; DB 7; Length 325;

Best Local Similarity 22.4%; Pred. No. 15;

Matches 28; Conservative 15; Mismatches 44; Indels 38; Gaps 5;

Qy 13 WSLVLLLLGLVMPALAIQAQLVLSYKEAVLRAIDGINQRSSDANLYRLDLDPRPTMGDPDP 72

Db 165 WALILLIL-----LALTIISYGVVV-----YNQLQTSNKTEL-----S 199

Qy 73 TPKPVSVFTVETVCPRTTQSPEDCDPKQGLVKRCMGTVTLNQARSGFDISCDKDKRFP 132

Db 200 TSTKSKDKTKDANSTTQSOTSITTFADGG-----NNITLSNTNGKVEVT-----F 246

Qy 133 ALLGCD 137

Db 247 TLTGCD 251

RESULT 10

US-11-192-967-2

; Sequence 2, Application US/11192967

; Publication No. US20050262587A1

; GENERAL INFORMATION:

; APPLICANT: Flannagan, Ronald D.

; APPLICANT: Mathis, John P.

; APPLICANT: Meyer, Terry E.

; TITLE OF INVENTION: Novel Bt Toxin Receptors From

; TITLE OF INVENTION: Lepidopteran Insects and Methods of Use

; FILE REFERENCE: 35718/204664

; CURRENT APPLICATION NUMBER: US/11/192,967

; CURRENT FILING DATE: 2005-07-29

; PRIOR APPLICATION NUMBER: US/09/715,909

; PRIOR FILING DATE: 2000-11-17

; PRIOR APPLICATION NUMBER: 60/166,285

; PRIOR FILING DATE: 1999-11-18

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1717

; TYPE: PRT

; ORGANISM: Ostrinia nubilalis

US-11-192-967-2

Query Match 7.2%; Score 63; DB 7; Length 1717;

Best Local Similarity 19.7%; Pred. No. 1.6e+02;

Matches 28; Conservative 24; Mismatches 52; Indels 38; Gaps 5;

Qy 5 RDGHSGLGRWSLVLL-----LGLVMPALAIQAQLVLSYKEAVLRAIDGINQRSSDANLYRL 59

Db 118 RQNEADQWLSLVITQRQDYETATMQSYVFSIQVGESEQVLLVALEIVN----- 165

Qy 60 DLDPRTMGDPDPKPVSVFTVETVCPRTTQSPEDCDPK---KQGLVKRCMGTVTLNQ 116

Db 166 -----IDNPN-----PILQVWSACVPIPEHGEARLTDVCYQVSDRDGGEISRTFRVDS 214

Qy 117 ARGSFDISCDKDKRFPALLGDP 138

Db 215 SRAA-----DESIFYMWGEY 229

RESULT 11

US-11-193-715-2

; Sequence 2, Application US/11193715

; Publication No. US20050260675A1

; GENERAL INFORMATION:

; APPLICANT: Flannagan, Ronald D.

; APPLICANT: Mathis, John P.

; APPLICANT: Meyer, Terry E.

; TITLE OF INVENTION: Novel Bt Toxin Receptors From

; TITLE OF INVENTION: Lepidopteran Insects and Methods of Use

; FILE REFERENCE: 35718/204664

; CURRENT APPLICATION NUMBER: US/11/193,715

```
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/09/715,909
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,285
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1717
; TYPE: PRT
; ORGANISM: Oestrinia nubilalis
US-11-193-715-2

Query Match          7.2%; Score 63; DB 7; Length 1717;
Best Local Similarity 19.7%; Pred. No. 1.6e+02;
Matches 28; Conservative 24; Mismatches 52; Indels 38; Gaps 5;

QY  5 RDGSLGRWSLVLL-----LGLVMPLAIQAQLVLSYKEAVLRRAIDGINQRSSDANLYRLL 59
DB 118 RQNEADGGWSLVITQRQYETATMQSYVFSIQVEGESQAVLVALIVN----- 165

QY  60 DLDPRPTWDGPDTPKPVSVFTVKETVCPRTTQQSPEDCDFK---KQGLVKRCMGVTVLNQ 116
DB 166 -----IDNP-----PILQVVSACVPIEHGEARLTDCVYQVSDRDGEISTREMTFRVDS 214

QY 117 ARGSFDISCDKDKRFPALLGDF 138
DB 215 SRAA-----DESIFYMVGEY 229

RESULT 12
US-11-012-762-8
; Sequence 8, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Georgia State University Research Foundation, Inc.
; FILE REFERENCE: GSU1.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 874
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-762-8

Query Match          7.1%; Score 62.5; DB 7; Length 874;
Best Local Similarity 26.3%; Pred. No. 69;
Matches 20; Conservative 11; Mismatches 28; Indels 17; Gaps 2;

QY  94 PEDCDFDK-----GLVKRCMGVTVLNQARGSFDISCDKDKRFPALLGDF 138
DB 678 PKDFDSEGLSVSGNGGAPEQQVAGAVLDLMDGEAQNMSRQQQLKWRDKKRP--VQQS 735

QY 139 FRKSKBKIKGFKRIV 154
DB 736 QQEDKKIKTESGRFI 751

RESULT 13
US-11-033-365-198
; Sequence 198, Application US/11033365
; Publication No. US20050250678A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
```

```
; APPLICANT: Wang, ZhiGuang
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: O-Linked Glycosylation of peptides
; FILE REFERENCE: 040853-01-5138
; CURRENT APPLICATION NUMBER: US/11/033,365
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,284
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 60/544,411
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/546,631
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/555,813
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: 60/570,891
; PRIOR FILING DATE: 2004-05-12
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-365-198

Query Match          7.1%; Score 62; DB 7; Length 192;
Best Local Similarity 25.7%; Pred. No. 9.6;
Matches 39; Conservative 24; Mismatches 37; Indels 52; Gaps 10;

QY 14 SLVLLGLVMPLAIQAQLVLSYKEAV--LRAI--DGINQRSSDANLYRLL-DLDRPTMD 68
DB 73 NELLRLISLLL-----IQSWLFPVQLRSVFANSIVYGASDSNVYLLKDL-----E 120

QY  69 GDDPTPKPVSVFTVKETVCPRTTQQSPEDCDFKQGLVKRCMGVTVLNQARGSFDISCDK 128
DB 121 G-----IQTLGRLDGSPPT-----TQIFKQTSYKFDNTHND 154

QY 129 NKRFPALLGDF-----FRKSKBKIKGFKRIVQ 155
DB 155 D---ALLKNYGLLYCFRQMDKV-ETFLRIVQ 182

RESULT 14
US-11-033-365-200
; Sequence 200, Application US/11033365
; Publication No. US20050250678A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Wang, ZhiGuang
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: O-Linked Glycosylation of peptides
; FILE REFERENCE: 040853-01-5138
; CURRENT APPLICATION NUMBER: US/11/033,365
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,284
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 60/544,411
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/546,631
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/555,813
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: 60/570,891
; PRIOR FILING DATE: 2004-05-12
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-365-200
```


November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications_databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_NA_Main) and **.rapbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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